

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 16:08:57 ; Search time 2886.99 Seconds
(without alignments)
4327.146 Million cell updates/sec

Title: us-08-816-011c-1
Perfect score: 2441
Sequence: 1 acgcgacgcgcgcgagtgta.....atctgattcgtcgctcgag 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_ph: *
6: gb_pl1: *
7: gb_pl2: *
8: gb_pr1: *
9: gb_pr2: *
10: gb_pr3: *
11: gb_ro: *
12: gb_sy: *
13: gb_un: *
14: em_fun: *
15: em_hum1: *
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17: em_in: *
18: em_om: *
19: em_or: *
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78: gb_hcg25: *
79: gb_hcg26: *
80: gb_hcg27: *
81: gb_hcg28: *
82: gb_hcg29: *
83: gb_hcg30: *
84: gb_hcg31: *
85: gb_hcg32: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2441	100.0	2441	81	126670 Sequence 1
2	2371.8	97.2	3568	32	DMU55321
3	1282.2	52.5	21163	58	AC013909 Drosophila
4	1282.2	52.5	314087	30	AE003484 Drosophila
5	165.2	6.8	33463	57	AC012766 Drosophila
6	57.8	2.4	1887	11	AF006824 Mus muscu
7	56.2	2.3	897	11	AF022821 Mus muscu
8	56.2	2.3	1888	11	AB008537 Mus muscu
9	56.2	2.3	2009	11	AB013345 Mus muscu
10	55.6	2.3	321	51	AX003049 Sequence
11	55.6	2.3	1236	10	AF129399 Homo sapi
12	55.6	2.3	1246	51	AX003047 Sequence
13	55.6	2.3	1252	34	AF171068 Homo sapi
14	55.6	2.3	2106	10	AF004711 Homo sapi
15	54.6	2.2	2077	11	AF031384 Rattus no
16	54.6	2.2	2772	34	AF247042 Homo sapi
17	53.4	2.2	2590	10	AF006823 Homo sapi
18	53.2	2.2	2730	34	AF279890 Homo sapi
19	52.4	2.1	1794	11	AX018705 Sequence
20	52.4	2.1	1795	11	AF056492 Mus muscu
21	52.2	2.1	1993	11	AX018706 Sequence

22	52.2	2.1	1994	11	AX003051	Sequence	
23	52.2	2.1	3580	11	MMU73488	U73488 Mus musculus	
24	51.6	2.1	1854	11	AF196965	AF196965 Rattus no	
25	49	2.0	1017	34	AF281302	AF281302 Homo sapi	
26	49	2.0	2180	51	AX020359	AX020359 Sequence	
27	49	2.0	2180	81	A94721	A94721 Sequence 1	
28	49	2.0	2649	10	AF134149	AF134149 Homo sapi	
29	49	2.0	2671	10	AF117708	AF117708 Homo sapi	
30	48.6	2.0	1219	30	AB036345	AB036345 Drosophil	
31	48.6	2.0	37888	59	AC017571	AC017571 Drosophil	
32	48.6	2.0	71457	30	AC005655	AC005655 Drosophil	
33	48.6	2.0	232156	30	AE003819	AE003819 Drosophil	
34	47.6	2.0	47518	60	AC020452	AC020452 Drosophil	
35	47.6	2.0	76743	30	AC005473	AC005473 Drosophil	
36	47.6	2.0	79114	54	AC005475	AC005475 Drosophil	
37	47.6	2.0	168301	37	AC007302	AC007302 Drosophil	
38	47.6	2.0	263411	30	AE003838	AE003838 Drosophil	
39	47.4	1.9	2332	34	AK022344	AK022344 Homo sapi	
40	46.8	1.9	1125	34	AF212829	AF212829 Homo sapi	
41	46.8	1.9	1125	34	AF279809	AF279809 Homo sapi	
42	46.8	1.9	1158	11	AF212827	AF212827 Cavia por	
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44	45.4	1.9	1860	53	HSU76996	U76996 Homo sapien	
45	45.4	1.9	1882	53	HS033632	U33632 Human two P	

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26	49	2.0	2180	51	AX020359	AX020359 Sequence	
27	49	2.0	2180	81	A94721	A94721 Sequence 1	
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29	49	2.0	2671	10	AF117708	AF117708 Homo sapi	
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32	48.6	2.0	71457	30	AC005655	AC005655 Drosophil	
33	48.6	2.0	232156	30	AE003819	AE003819 Drosophil	
34	47.6	2.0	47518	60	AC020452	AC020452 Drosophil	
35	47.6	2.0	76743	30	AC005473	AC005473 Drosophil	
36	47.6	2.0	79114	54	AC005475	AC005475 Drosophil	
37	47.6	2.0	168301	37	AC007302	AC007302 Drosophil	
38	47.6	2.0	263411	30	AE003838	AE003838 Drosophil	
39	47.4	1.9	2332	34	AK022344	AK022344 Homo sapi	
40	46.8	1.9	1125	34	AF212829	AF212829 Homo sapi	
41	46.8	1.9	1125	34	AF279809	AF279809 Homo sapi	
42	46.8	1.9	1158	11	AF212827	AF212827 Cavia por	
43	45.4	1.9	1224	53	HSU090065	U90065 Human potas	
44	45.4	1.9	1860	53	HSU76996	U76996 Homo sapien	
45	45.4	1.9	1882	53	HS033632	U33632 Human two P	

22	52.2	2.1	1994	11	AX003051	Sequence	
23	52.2	2.1	3580	11	MMU73488	U73488 Mus musculu	
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25	49	2.0	1017	34	AF281302	AF281302 Homo sapi	
26	49	2.0	2180	51	AX020359	AX020359 Sequence	
27	49	2.0	2180	81	A94721	A94721 Sequence 1	
28	49	2.0	2649	10	AF134149	AF134149 Homo sapi	
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QY 1381 gatttgctggccaagtggttaacacgactggtgccaaggtggaagccaacggtggaagcag 1440
Db 1381 GATTTCGTGGCCCAAGTGGTCAACGCATTCGCGACGGTGAAGCCACCGCGCGGGAACAG 1440
QY 1441 gaagatgcggctctctatggtggtctatcatggtctctccgactccagatcctcgccagc 1500
Db 1441 GAAGATGCGGCTCTATGTTGGTGGCTATCATGGCTTCTCGACTCCAGATCTCTGCGCAGC 1500
QY 1501 gaatggtcgttctcagcaggttaacagagttcacatcacgcgcagctccaaagagcacgtgcc 1560
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QY 1621 cacaacgaatgacatgagcgcgacacacagcagatccagagagcattcaacacagcgc 1680
Db 1621 CACACGAATGACATGAGCGCGCACACACAGCAGATCCAGGAGCATTCACACGAGCGC 1680
QY 1681 tacaaggagcagcgtgtccaacggagcagccaactcgacatggtccatctggagcgc 1740
Db 1681 TACAAGGAGCAGCAGCGTCCCAACGGAGCAGCCAACTCGACCATGTCATCTGGAGCGC 1740
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Db 1741 GATGCTTTGGAGGAGCAGCTGAGAACAATACCGGGTGCCTGCGCTCAAGAAAGTTCT 1800
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QY 1861 tggagcgaagtgttcggtcgttaccgcgaggggtgtcatctcgcaggaagcagat 1920
Db 1861 TGGAGCGCAAGTGTTCGCTGGTACCGAGGGTGTCTATCTCGCAGGAAGCCAGAT 1920
QY 1921 cccctgagactactacatcaacaggttcacagcgagcggtccagtcacttattgagca 1980
Db 1921 CCCCCTGGACTACTACATCAACAGCGGTACCGCGGCTTCCAGTCAATCTTATTTTCGCA 1980
QY 1981 acgagcggttcgcacgccttcgaaatgaatgagcagcttgccagcgagcgcgcg 2040
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Db 2041 GGTAAACGAACATGGGCTTCCAGATGGAGGATGGAGCAACCCGCCCATCGGCATTTGGCG 2100
QY 2101 gtgagcctatacaacgaagcggtgctggaagcgccagcgagagcagcatctacacc 2160
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Db 2161 AGAATCAAGCCCATCCGCTCCGCGGCGAGCATGTATCCGCGGACCGCGCATCTTGG 2220
QY 2221 cccagatgcagatgcgaagcgagcgttggcaaccagtggtctctggaatcgcgccatgg 2280
Db 2221 CCCAGATGCAGATGCAGCGCGCAGCTTGGCAACCAAGTGGCTGGATCGCGCGGCATGG 2280
QY 2281 cggagatgagcgcgctggtgagcagcctctccagctacagatcggcatacgcgtga 2340
Db 2281 CGGAGTGGCGCGCGCTGTGTGCGACGCCCTTCCAGCTACAGCATCGCATCATCGCTGA 2340
QY 2341 cctctgctcgcgcgaagcagcatattctcgtttacctccgaaagagatgaatgtgc 2400
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QY 2401 tggagcagacgaccattgctggtatctgattcgtgctcgag 2441
Db 2401 TGGAGCAGACGACCATTCGGGATCTGATTCTGTGCGCTCGAG 2441
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RESULT 2
DMU55321 3568 bp mRNA INV 29-OCT-1998
Drosophila melanogaster two P domain potassium channel ORK1 (ORK1)
mrna, complete cds.
U55321
U55321.1 GI:3808067
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 3568)
Goldstein, S.A., Price, L.A., Rosenthal, D.N. and Pausch, M.H.
ORK1, a potassium-selective leak channel with two pore domains
cloned from Drosophila melanogaster by expression in Saccharomyces
cerevisiae
Proc. Natl. Acad. Sci. U.S.A. 93 (23), 13256-13261 (1996)
97075152
2 (bases 1 to 3568)
Goldstein, S.A.N., Price, L.A., Rosenthal, D.N. and Pausch, M.H.
Direct Submission
Submitted (17-APR-1996) S.A.N. Goldstein, Pediatrics and Cellular
and Molecular Physiology, Yale University School of Medicine, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA
3 (bases 1 to 3568)
Goldstein, S.A.N., Price, L.A., Rosenthal, D.N. and Pausch, M.H.
Direct Submission
Submitted (29-OCT-1998) S.A.N. Goldstein, Pediatrics and Cellular
and Molecular Physiology, Yale University School of Medicine, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA
REMARK
Sequence update by submitter
On Oct 29, 1998 this sequence version replaced gi:1666502.
COMMENT
Location/Qualifiers
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/dev_stage="third instar larva; adult"
/chromosome="1"
/map="10A1-2"
/tissue_type="brain and muscles of adults"
<1. 3568
/gene="ORK1"
189. 3194
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rectifier/leak potassium channel"
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/product="two P domain potassium channel ORK1"
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GFGDYPTFGANQPKFGGFWVQIFVIVWFIFSLGYLVNIMFITRGLQSKLAVL
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STMVHLEPDLLEOLKKKSPGACRVKFPMPDGLRLFPFOKPSODLERKLSVVS
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MEDGATPPSALGGGAYORKAAGRRRESIYTONQAPSARGSMYPTPAHALAQMOMR
RGLSATSGSAAWAAVAAARGSLFPATASASSUTSAPRRSISFVTSKEDMNVLEPT
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813 a 1038 c 949 g 768 t
BASE COUNT

KIQYSLPIMIPDLSTDCVESHSSPGGGGRYSDTPSPHCLCSCQTSQTSVSTG
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2009

polyA_site

BASE COUNT 328 a 687 c 607 g 387 t

ORIGIN

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Best Local Similarity 58.8%; Pred. No. 0.0083;
Matches 97; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 456 gtgagaccttaccatgccttcttcttccgcttcacgcgttgcctccacggtgggatagg 515
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Db 426 TCATGCGCGCCGCCAGCAGCAGGAGCAAGGTGTTCTGCATGTTCTACGCGCTGCTGGG 485
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QY 576 catcccgctcaatggatcctcttcttccgcttcgctcggaatactt 620
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RESULT 10
AX003049 321 bp DNA PRI 24-AUG-2000
LOCUS
DEFINITION Sequence 3 from Patent WO9937762.
ACCESSION AX003049
VERSION AX003049.1 GI:9926935
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Chapman,C.G. and Meadows,H.J.
TITLE Trek-1 like two pore potassium channel
JOURNAL Patent: WO 9937762-A 29-JUL-1999;
SMITHKLINE BEECHAM PLC (GB).
FEATURES
source
1. .321
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 86 a 67 c 66 g 102 t

ORIGIN

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Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 471 tgctcttcttgccttcacgcgttgcctccacggtgggatattcgcccaac 530
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Db 39 TTCCTTCTTCTTTCGTCGGCAGTATTATACACCATAGGATTTGGAACATCTCACCAG 98
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QY 531 cactctcgccgagcagatgatcatgcgtattcggatggcattcccgatcaatgg 590
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Db 99 CACAGAGCGCGGCAAAATATCTGATCATCTATGCTTACTGGGAATTCCTCTTTGG 158
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QY 591 tatctcttgcgctcgccggaatactttggacgtacgtttgaa 636
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Db 159 TTTTCTCTTGGCTGGAGTTGGAGATCAGCTAGGCACCATATTGGA 204
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RESULT 11
AF129399 1236 bp mRNA PRI 09-AUG-1999
LOCUS
DEFINITION Homo sapiens TREK-1 potassium channel (KCNK2) mRNA, complete cds.
ACCESSION AF129399
VERSION AF129399.1 GI:5712620
KEYWORDS

SOURCE
ORGANISM

human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1236)
AUTHORS Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and
Lazdunski,M.
TITLE Inhalational anaesthetics are activators of two pore domain
background K+ channels
JOURNAL Nat. Neurosci. (1999) In press
REFERENCE 2 (bases 1 to 1236)
AUTHORS Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and
Lazdunski,M.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-1999) IPMC, CNRS, 660 route des lucioles, Sophia
Antipolis, Valbonne 06560, France
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/product="TREK-1 potassium channel"
/protein_id="AAD47569.1"
/db_xref="GI:5712621"
/translation="MAAPDLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKWK
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WILVGLAYFAAVLSMIGDWRVISKKEEVEGFRAHAAEWTANYAEKFKRRRLSV
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BASE COUNT 330 a 279 c 299 g 328 t

ORIGIN

Query Match 2.3%; Score 55.6; DB 10; Length 1236;
Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Db 393 TTCCTTCTTCTTTCGTCGGCAGTATTATACACCATAGGATTTGGAACATCTCACCAG 452
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QY 531 cactctcgccgagcagatgatcatgcgtattcggatggcattcccgatcaatgg 590
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 453 CACAGAGCGCGGCAAAATATCTGATCATCTATGCTTACTGGGAATTCCTCTTTGG 512
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QY 591 tatctcttgcgctcgccggaatactttggacgtacgtttgaa 636
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Db 513 TTTTCTCTTGGCTGGAGTTGGAGATCAGCTAGGCACCATATTGGA 558
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RESULT 12
AX003047 1246 bp DNA PRI 24-AUG-2000

LOCUS

DEFINITION Sequence 1 from Patent WO9937762.
ACCESSION AX003047
VERSION AX003047.1 GI:9926934
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Chapman,C.G. and Meadows,H.J.

Trek-1 like two pore potassium channel
Patent: WO 937762-A 29-JUL-1999;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
source
1. .1246
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 335 a 280 c 302 g 329 t
ORIGIN

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Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 471 tgccttcttcttcgctccacggttgcacggtgggatggaatatatcgccaac 530
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Db 401 TTCCTCTCTCTTCTGCGCACTGTTATTACAAACCATAGGATTGGAAACATCTCACCACG 460
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Qy 531 caccctgcgcgagcagatgatcgcggtatcggtgattcggtgacatcccgccaatgg 590
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Db 461 CACAGAAGGGGGGAAAAATATCTGATCATCTATGCTTACTGCGAATTCCTCTTTGG 520
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RESULT 13
AF171068
LOCUS AF171068 1252 bp mRNA PRI 01-AUG-2000
DEFINITION Homo sapiens two-pore domain potassium channel TREK-1 (TREK-1)
mRNA, complete cds.
ACCESSION AF171068
VERSION AF171068.1 GI:9622334
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1252)
AUTHORS Meadows,H.J., Benham,C.D., Cairns,W., Gloger,I.S., Jennings,C.,
Meadhurst,A.D., Murdoch,P. and Chapman,C.G.
TITLE Cloning, localization and functional expression of the human
ortholog of the TREK-1 potassium channel
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1252)
AUTHORS Chapman,C.G., Gloger,I.S. and Meadows,H.J.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1999) Biotechnology & Genetics, SmithKline
Beecham Pharmaceuticals, New Frontiers Science Park (North), Third
Avenue, Harlow, Essex CM19 5AW, UK
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1. .1252
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/note="KCNK2"
15. .1250
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Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Qy 531 caccctgcgcgagcagatgatcgcggtatcggtgattcggtgacatcccgccaatgg 590
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Db 467 CACAGAAGGGGGGAAAAATATCTGATCATCTATGCTTACTGCGAATTCCTCTTTGG 526
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RESULT 14
AF004711
LOCUS AF004711 2106 bp mRNA PRI 05-JAN-1999
DEFINITION Homo sapiens two-pore potassium channel TP KC1 mRNA, complete cds.
ACCESSION AF004711
VERSION AF004711.1 GI:4101565
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2106)
AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.
TITLE TP KC1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2106)
AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-1997) Cyanamid Agricultural Research Center,
American Cyanamid Company, PO Box 400, Princeton, NJ 08543-0400,
USA.
FEATURES
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154. .1434
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BASE COUNT 552 a 471 c 486 g 581 t 16 others
ORIGIN

Query Match 2.3%; Score 55.6; DB 10; Length 2106;
Best Local Similarity 58.4%; Pred. No. 0.012;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 471 tgccttcttcttcgctccacggttgcacggtgggatggaatatatcgccaac 530

GenCore version 4.5
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OM nucleic : nucleic search, using sw model

Run on: March 17, 2001, 16:11:22 ; Search time 122.06 Seconds
(without alignments)
7512.638 Million cell updates/sec

Title: US-08-816-011c-1
Perfect score: 2441
Sequence: 1 acgcagccgcgcgagtgta.....atctgattcgtgcgtcgag 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2441	100.0	2441	17 T33201	DmORF1 potassium c
2	55.6	2.3	321	20 Z00041	Partial h-TREK1 po
3	55.6	2.3	1246	20 Z00039	h-TREK1 polynucleo
4	55.6	2.3	3300	20 Z11915	Human potassium ch
5	54.6	2.2	1182	21 A27105	Human h-TAAK cDNA
6	54.6	2.2	1218	21 A27106	Human h-TAAK cDNA
7	53.4	2.2	1551	21 Z98176	Human signal pepti
8	52.4	2.1	1794	20 Z10606	cDNA encoding a me
9	52.2	2.1	1993	20 Z10607	cDNA encoding a me
10	52.2	2.1	1994	20 Z10607	Mouse h-TREK1 poly
11	49	2.0	2180	20 Z00040	Human hTREK-1 cDNA
12	49	2.0	2571	20 Z11914	Human potassium ch

13	49	2.0	2671	21	246092	cDNA encoding KT4,
14	49	2.0	2735	21	246094	cDNA encoding KT5,
15	45.4	1.9	1894	18	T64960	Twik-1 potassium c
16	41.8	1.7	1011	17	T33202	F22b7.7 potassium
17	41	1.7	3480	21	A07601	Long QT syndrome a
18	41	1.7	3950	21	A07602	Long QT syndrome a
19	41	1.7	10732	21	A10594	Gene encoding a su
20	40.6	1.7	1497	21	A15943	Human protein clon
21	40.6	1.7	3768	21	A15953	Human MAP cDNA cl
22	39.2	1.6	1658	21	Z87209	Human erg subfamil
23	38.8	1.6	3141	20	X56415	Plasmid pMP76 DNA.
24	37.8	1.5	12474	20	X78131	Rat eikl potassium
25	37.6	1.5	3742	21	Z93334	Human colon cancer
26	36.8	1.5	756	21	A02602	Human ischaemic he
27	36.6	1.5	1981	21	Z51194	Gene No. 20 encodi
28	36.6	1.5	2017	20	V08830	Human DNA encoding
29	36.4	1.5	1801	21	A09381	Human potassium ch
30	36.4	1.5	3424	20	Z11901	Human gene signatu
31	36	1.5	296	16	T25865	Mycobacteriophage
32	36	1.5	49272	19	V35000	3-acylating enzyme
33	35.8	1.5	2381	15	Q44449	Mouse KCNQ3 cDNA.
34	35.8	1.5	2814	20	X57141	Human potassium io
35	35.8	1.5	2886	21	Z35716	Human potassium io
36	35.8	1.5	2967	21	Z35717	Human eag related
37	35.8	1.5	3002	21	Z35721	Human eag related
38	35.8	1.5	3083	21	Z35722	Total DNA sequence
39	35.8	1.5	30001	18	T61016	S. aureofaciens DN
40	35.8	1.5	30001	20	X05110	Leishmania antigen
41	35.6	1.5	516	19	V47574	cDNA encoding huma
42	35.6	1.5	1170	21	A23431	Human brain Expres
43	35.4	1.5	348	14	Q61357	Human ischaemic he
44	35.4	1.5	2008	21	Z51193	Partial FRAXE regi
45	35.4	1.5	2974	16	Q79630	

ALIGNMENTS

RESULT 1	
T33201	
ID	T33201 standard; cDNA; 2441 BP.
XX	
AC	T33201;
XX	
DT	16-OCT-1996 (first entry)
XX	
DE	DmORF1 potassium channel gene.
XX	
KW	DmORF1; potassium channel; fruitfly; polyadenylation site;
KW	potassium dependence; Saccharomyces cerevisiae; potassium-agonist;
KW	potassium-antagonist; drug screening; insecticide; cardiac disorder;
SS	ss.
OS	Drosophila melanogaster.
XX	
FH	Key Location/Qualifiers
CDS	190..2046
FT	/*tag= a
FT	/product= Potassium channel DmORF1 protein
FT	polyA_signal 2093..2098
FT	/*tag= b
XX	
PN	WO9613520-A1.
XX	
PD	09-MAY-1996.
XX	
PF	25-OCT-1995; 95WO-US14364.
XX	
PR	31-OCT-1994; 94US-0332312.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
XX	
PI	Pausch MH, Price LA;


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Db 1681 tacaaggacagcagcgtgccaacgagcagcgaactgcacatggtccatctggagcgg 1740
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RESULT 2

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ID Z00041 standard; DNA; 321 BP.
XX
AC Z00041;
XX
DT 12-OCT-1999 (first entry)
XX
DE Partial h-TREK1 polynucleotide.
XX
KW partial h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome lq32; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..321
FT /tag= a
FT /product= "partial h-TREK1 polypeptide"
FT /transl_except= (pos:4..6, aa:Ser)
FT /transl_except= (pos:13..15, aa:Val)
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XX WO9937762-A1.
PN
XX 29-JUL-1999.
PD
XX 02-DEC-1998; 98WO-EP07805.
PF
XX 09-OCT-1998; 98GB-0022135.
PR
XX 27-JAN-1998; 98EP-0300570.
PR
XX (SMIK ) SMITHKLINE BEECHAM PLC.
PA
XX Chapman CG, Meadows HJ;
PI
XX WPI; 1999-469126/39.
DR
XX P-PSDB; Y28498.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
PT pulmonary, cardiovascular and inflammatory diseases
XX
PS Claim 18; Page 24; 44pp; English.
XX
CC This sequence is a partial h-TREK1 polynucleotide, encoding the h-TREK1
CC polypeptide Y28498. Z00039 and Y28496 are complete h-TREK1 polynucleotide
CC and polypeptide sequences. h-TREK1 is a two pore potassium channel, and
CC the gene maps to human chromosome lq32, between the markers D15237 and
CC W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC disease or susceptibility to a disease related to expression or activity
CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC treatment of diseases including cancer, pulmonary, cardiovascular, and
CC inflammatory diseases, pain, psychiatric disorders, including depression
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC stroke, and head trauma and neurological disorders including migraine.
XX
SQ Sequence 321 BP; 86 A; 67 C; 66 G; 102 T; 0 other;
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Query Match 2.3%; Score 55.6; DB 20; Length 321;
Best Local Similarity 58.4%; Pred. NO. 9.4e-06;
Matches 97; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Qy 531 cacttcgccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 590
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Qy 591 tatectcttgcggcctcgcgaatactttggacgtacgtttgaa 636
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RESULT 3

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200039
ID Z00039 standard; DNA; 1246 BP.
XX
AC Z00039;
XX
DT 12-OCT-1999 (first entry)
XX
DE h-TREK1 polynucleotide.
XX
KW h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome lq32; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..1244
FT /tag= a
FT /product= "h-TREK1"
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[illegible]

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Db	780	ggtcgtgagagtgctgcgcagtgctcttctcctgctgctgctgcctgctcttctgtcc	839
Qy	755	tgggtcgcctgcgtgggtgttcacactacttcgagaactggcctatcttccatctgc	814
Db	840	t-----cactcctacctcgtgttctcctacatggagagctggagcaagttagaagccatc	895
Qy	815	tgtactacagctatgtgacccacacacaaatggattcggatcgtatgtgccacatttg	874
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Db	954	gcaccgggcagaaactctcagactaccagccgctggctgggttctggatctgtttggcc	1013
Qy	935	tgtggttcactctctctcgtcg	954
Db	1014	tagcctactcgcctcagtg	1033
RESULT	9		
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XX	Z10607 standard; CDNA; 1993 BP.		
AC	Z10607;		
XX	18-NOV-1999 (first entry)		
DE	CDNA encoding a mechanically sensitive potassium channel protein TREK-		
XX	Mechanically sensitive potassium channel protein; TREK-1;		
KW	polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;		
KW	nervous system disease; epilepsy; cardiovascular disease; arrhythmia;		
KW	neurodegeneration; ischemia; anoxia; hormone secretion abnormality;		
KW	muscular disease; ds.		
OS	Mus sp.		
XX			
FH	Key	Location/Qualifiers	
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FT		/*tag= a	
XX			
PN	W09945108-A2.		
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PD	10-SEP-1999.		
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PF	23-FEB-1999;	99WO-FR00404.	
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PR	05-MAR-1998;	98FR-0002725.	
XX			
PA	(CNRS) CNRS CENT NAT RECH SCI.		
XX			
PI	Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;		
XX			
DR	WPI; 1999-551038/46.		
DR	P-PSDB; Y30648.		
XX			
PT	New mechanically sensitive potassium channel, used to screen for		
PT	specific modulators, potential therapeutic agents for heart and nervous		
PT	system disorders		
XX			
PS	Claim 7; Page 23-25; 40pp; French.		
XX			
CC	The present sequence encodes a mechanically sensitive potassium		
CC	channel protein designated TREK-1. The protein is activated by		
CC	polyunsaturated fatty acids, particularly arachidonic acid, and by		
CC	riluzole. The protein is used to screen for specific modulators which		
CC	are useful for treating or preventing diseases of the heart and nervous		
CC	systems in humans and animals, e.g. epilepsy, cardiovascular disease		
CC	(arrhythmia), neurodegeneration (particularly where associated with		

CC certain renal, cardiovascular and central nervous system (CNS) disorders.
CC Nucleotides encoding K-Hnov proteins may be used for identifying
CC homologous or related proteins and the DNA sequences encoding them. They
CC may be used to produce compositions that modulate the expression and
CC function of the K-Hnov protein and in studying the biochemical pathways
CC associated with it. They may also be used for the recombinant production
CC of K-Hnov protein in fermentation cultures. Additionally, such
CC nucleotides may be used in gene therapy protocols for the treatment
CC of diseases associated with abnormal potassium channels.
XX
XX

Sequence 2571 BP; 488 A; 744 C; 774 G; 565 T; 0 other;

Query Match 2.0%; Score 49; DB 20; Length 2571;
Best Local Similarity 55.6%; Pred. No. 0.0018;
Matches 94; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 446 cgccctacacgtggaaccttaccatgcctcttcttcgcttcacgcgtttgtccacgg 505
DB 369 cggaccgccgtggacttcgctctgctctcttcttcgacgacgtgatcaccacgg 428
QY 506 tgggatgggaatatatcccaacccttcgacgacgacgatcatatcgcgatt 565
DB 429 tgggctatgggtacacacgcactgactgatgcgggcaaggcttctccatgcgtttg 488
QY 566 cgggtgattggcatcccgctcaatggatcctcttgcggcctcgcgga 614
DB 489 cgctcctggcggtgcgacacacatgctgctgctgacccgctcagccca 537

RESULT 13

Z46092
ID Z46092 standard; cDNA; 2671 BP.

AC Z46092;

DT 05-MAY-2000 (first entry)

DE cDNA encoding KT4, a TWIK family 2PD potassium channel polypeptide.

XX KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; AA604914; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 111..1052
FT CDS /*tag= a
FT /*product= "KT4"

XX WO200003687-A2.

XX 27-JAN-2000.

XX 20-JUL-1999; 99WO-US16471.

XX 20-JUL-1998; 98US-0093486.

XX 13-AUG-1998; 98US-0096655.

XX (ELAN-) ELAN PHARM INC.

XX Forsayeth JR, Zhao BB, Chavez RA;

XX WPI; 2000-171196/15.

XX P-PSDB; Y68737.

XX Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -

PS Claim 14; Fig 1A-C; 53pp; English.

XX The present sequence encodes a protein, designated KT4, which is a
XX member of the TWIK family 2PD potassium channel polypeptides. These
XX polypeptides contain two potential P-domains and 8 (preferably 4)
XX transmembrane domains. The KT4 cDNA sequence was isolated from a brain
XX cDNA library using degenerate oligonucleotides derived from human
XX expressed sequence tag (EST) AA604914. The polypeptides and
XX polynucleotides are used in the diagnosis, prevention and treatment of
XX disease states. The polynucleotides may be used to detect and
XX quantitate expression of TWIK family 2PD potassium channels, and
XX aberrant or mutant forms of the polynucleotide which cause various
XX diseases and disorders. Antisense oligonucleotides may be used to
XX modulate the expression of polynucleotides of the invention. The
XX polypeptides are used for treating diseases and disorders associated
XX with ion channel dysfunction, including renal, musculoskeletal and
XX proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
XX dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
XX and cancers.

Sequence 2671 BP; 563 A; 743 C; 798 G; 567 T; 0 other;

Query Match 2.0%; Score 49; DB 21; Length 2671;
Best Local Similarity 55.6%; Pred. No. 0.0018;
Matches 94; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

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DB 370 cggaccgccgtggacttcgctctgctctcttcttcgacgacgtgatcaccacgg 429
QY 506 tgggatgggaatatatcccaacccttcgacgacgacgatcatatcgcgatt 565
DB 430 tgggctatgggtacacacgcactgactgatgcgggcaaggcttctccatgcgtttg 489
QY 566 cgggtgattggcatcccgctcaatggatcctcttgcggcctcgcgga 614
DB 490 cgctcctggcggtgcgacacacatgctgctgctgacccgctcagccca 538

RESULT 14

Z46094
ID Z46094 standard; cDNA; 2735 BP.

XX Z46094;

DT 05-MAY-2000 (first entry)

XX cDNA encoding KT5, a TWIK family 2PD potassium channel polypeptide.

XX KT5; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; AA533124; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 123..1064
FT CDS /*tag= a
FT /*product= "KT5"

XX WO200003687-A2.

XX 27-JAN-2000.

XX 20-JUL-1999; 99WO-US16471.

XX 20-JUL-1998; 98US-0093486.

XX 13-AUG-1998; 98US-0096655.

XX (ELAN-) ELAN PHARM INC.

Search completed: March 17, 2001, 17:56:23
Job time: 6301 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 16:09:57 ; Search time 71.04 Seconds
(without alignments)
5537.617 Million cell updates/sec

Title: US-08-816-011C-1
Perfect score: 2441
Sequence: 1 acgcgacgcgcgcgagtga.....atctgattctgcgtcgaq 2441

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database : Issued_Patents_NA:**
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTRUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/BACKFILES1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description
		Match	Length		
1	2441	100.0	2441	1	Sequence 1, Appli
2	45.4	1.9	1894	3	Sequence 1, Appli
3	41.8	1.7	1011	1	Sequence 3, Appli
4	38.8	1.6	3141	2	Sequence 1, Appli
5	38.8	1.6	3141	3	Sequence 1, Appli
6	36	1.5	49272	1	Sequence 1, Appli
7	35.8	1.5	30001	1	Sequence 1, Appli
8	35.8	1.5	30001	2	Sequence 1, Appli
9	34.8	1.4	1881	2	Sequence 1, Appli
10	34.8	1.4	3041	2	Sequence 4, Appli
11	34.8	1.4	3718	2	Sequence 5, Appli
12	34.8	1.4	3796	2	Sequence 6, Appli
13	34.8	1.4	7218	1	Sequence 3, Appli
14	34.4	1.4	1317	3	Sequence 14, Appli
15	34.4	1.4	11517	1	Sequence 1, Appli
16	34.2	1.4	1260	1	Sequence 3, Appli
17	34	1.4	731	1	Sequence 2, Appli
18	34	1.4	3636	3	Sequence 2, Appli
19	33.8	1.4	720	3	Sequence 3, Appli
20	33.8	1.4	720	3	Sequence 3, Appli
21	33.8	1.4	720	3	Sequence 3, Appli
22	33.8	1.4	2338	1	Sequence 1, Appli
23	33.8	1.4	2338	2	Sequence 1, Appli
24	33.6	1.4	1001	3	Sequence 2, Appli
25	33.6	1.4	1112	3	Sequence 2, Appli
26	33.6	1.4	1772	2	Sequence 9, Appli
27	33.6	1.4	3243	2	Sequence 13, Appli
28	33.6	1.4	3243	2	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-332-312-1
: Sequence 1, Application US/08332312

PATENT NO. 9039620
GENERAL INFORMATION:
APPLICANT: price, Laura A.
APPLICANT: pausch, Mark H.
TITLE OF INVENTION: Functional Express
TITLE OF INVENTION: Melanagaster putat
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

```
% *****  
% COMPANY NAME: One Cyanamid Plaza  
% STREET:  
% CITY: Wayne  
% STATE: New Jersey  
% COUNTRY: US  
% ZIP: 07470-8426  
% COMPUTER READABLE FORM:  
% MEDIUM TYPE: Floppy disk  
% COMPUTER: IBM PC compatible  
% OPERATING SYSTEM: PC-DOS/WMS-DOS  
% SOFTWARE: Patent In Release #1.0, Version #1.25  
% CURRENT APPLICATION DATA:  
% APPLICATION NUMBER: US/08/332,312
```

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: P-38
REFERENCE/DOCKET NUMBER: 3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 190..2043
S-08-3332-312-1

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Query Match      100.0%; Score 2441; DB 1; Length 2441;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AC CGGATCGCGGAGTGATATATTTTTTTTATAGCTCAGTCTTTCAGTGTTCGCGATTCT 60
QY 61 ctttaaaagaaaaaataataagctcaaaactacaaaccacacagcgaagcgaag 120
Db 61 CTTTAAAGAAAAAATAAAGTCAAAACTAGAAACACACACAGCGAAGCGGAAAG 120
QY 121 caacggtctcgtcgagtggtttatTTTTTTTtttttcaaaatTTTTtgatcgtagtcgacaat 180
Db 121 CANCGGTCTCGAGTGTTATTTTTTTTTTTCACANAATTTTTGATCGTAGTCGGACAT 180
QY 181 ccgtcgagcatgtccgcgaatgatgatactctgctgtcctcatcttctacatatctcactcg 240
Db 181 CCGTCGAGCATGTCCGCGAATCATGATCGATCTCTGCTCATCTTCTACATATCTTACCTG 240
QY 241 atgttcggggcgcaatctattaccatattgaacacgagcggagagaagatatcgcgcgc 300
Db 241 ATGTTCCGGGCGGCAATCTATTACCATATTGAGCAGCGGAGGAGAGATATCGCGGCC 300
QY 301 gaacagcgcaagcgcaaatgcaatcaacgaatatctcgtcgagagctggcgagacaag 360
Db 301 GAACAGCGCAAGCGCAATTTGCAATCAACGAATATCTGCTGAGGAGCTGGCGACAAG 360
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Db 361 AATACGACCACACAGGATGAGATTCTTCAACGGATCTCGGATTACTGTGACAAACCGGTT 420
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Db 481 TTGCGCTTCACCGTTTGCTCCACGCTGGGATATGGGAATATATCGCCACACACCTTCGCC 540
QY 541 ggaagatgataatgcgctattcggtgattggcatcccccgaatggatcctctttt 600
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QY 601 gccgctcggaatactttgacatcagtttgaagcaatctacagacgtacaaaaag 660
Db 601 GCCGGCTCGGCGAATACTTTGACAGTACGTTTGAAGCGATCTACAGACGCTACAAAAAG 660
QY 661 tacaagatgccagcatatgcactatgtcccgcgcagctggattgatcacacggtg 720
Db 661 TACAAGATGCCAGCATATGCACTATGTCCCGCGCAGCTGGGATTGATCACCACGGTG 720
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QY 1561 tctccgatttcaatctggaggcacctcgtgagagcggagggccactcgtgttcgagc 1620
Db 1561 TGCTCCGATTTCAATCTGGAGGCACCTGCTGCGACAGCGAGAGGCCACTGCTGTCGAGC 1620
QY 1621 cacaacgaatgacatlggagcggcgacacaccagcagatccagagagcattcaaccagcgc 1680
Db 1621 CACAACGAATGGACATGGAGCGCGCAACACAGCAGATCCAGGAGCATTTCAACACAGCGC 1680
QY 1681 tacaaggacagcagcgtgccaaagcagcagcacaactcgaacatgctcatctcggagcgc 1740
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QY 1861 tggagcgaagtgttcctggttaccgagaggtgtcattctcgcaggaagccagat 1920
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QY 1921 ccccgctgactactacatacaacaggttcacgcgccctccagtcgaatcctctatttgcga 1980
Db 1921 CCCCCTGTGACTACTACATCAACACAGGTCACGCGGCGCTCCAGTCAATCTATTTCGGCA 1980
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QY 2041 ggctaagcaaatgggcttccagatggaggaatgggaacaccccgccatcggtatgggcg 2100
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QY 2101 gtygagctatacaacgcaaggcgtgtggycaagccgcgacgagagcatctacaccc 2160
Db 2101 GTGGAGCCTTATCAACGAAGCGGCTGTGTGGCAAGCGCGACGCGAGAGCATCTACACC 2160
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Db 2161 AGAATCAAGCCCCATCCGCTCGCGGGGAGCATGTATCCCGGACCGCGACGCGCTTGG 2220

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Qy 592 atctctttg 601
Db 1382 agcatcttcg 1391

RESULT 6

US-08-614-770A-1/c
; Sequence 1, Application US/08614770A
; Patent No. 5773267
; GENERAL INFORMATION:
; APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
; TITLE OF INVENTION: D29 SHUTTLE PHASMSIDS AND USES THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,770A
FILING DATE: MARCH 7, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/402
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49272
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: MYCOBACTERIOPHAGE
INDIVIDUAL ISOLATE: D29

US-08-614-770A-1

Query Match 1.5%; Score 36; DB 1; Length 49272;
Best Local Similarity 51.2%; Pred. No. 14;
Matches 84; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 1600 gagaggccactgcgttcagcacaacgaatggacatggagcgcagacacagcagatc 1659

Db 42506 GAGATCCCGATCCGGTTCAACTACAAAGGCACTCCGTCGTTGGAGAGATCGAAGACCC 42447

Qy 1660 cagaggcattcaaccagcgtacaaggagcagcagcgtgccaagcggagcagccaactcg 1719

Db 42446 CTCGAGCGGTACGAGCGGCTCTACGAGGACTTCCTCGCGCTGATCGTCTGGACAAATC 42387

Qy 1720 accatggtcatctggagccggatgctttggaggagcagctgag 1763

Db 42386 ACCAAGTCCCGACCGGATCGGGGACGGGATGACCCGTTTCAG 42343

RESULT 7

US-08-125-468-1
; Sequence 1, Application US/08125468
; Patent No. 5589385
; GENERAL INFORMATION:

APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracycline formation and cosmid
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,468
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-125-468-1

Query Match 1.5%; Score 35.8; DB 1; Length 30001;
Best Local Similarity 46.9%; Pred. No. 12;
Matches 112; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

Qy 756 ggtgctgcctcggtggtgttcaactacttcgagaactggggcctatcttccatctcgct 815

Db 10124 GGTGCTGCGGTGGGCGAGCGCGGTGAGATCCAGGTCCGGGCGCGGAGTGTGATCTGGG 10183

Qy 816 gtactacagctatgtgaccacacaaatggattcggtgactatgtgcccacatttgg 875

Db 10184 CTACCTGGCGACGGGCCACCGCGCTCGACGCGGACGCGCTGGTTCGCGACCGGTGA 10243

Qy 876 agcaaacagcccaaggaggttcggcggttctggtgtctatcagatctttgtatcgt 935

Db 10244 CGTCGGCGGATCGACGAGGCGCGCGCTGTGCTGTCGACCGGATCAAGAGCTTT 10303

Qy 936 gtggttcctctcgtcggtgatatcttctgtgatcattatcattatcactcggggcc 994

Db 10304 CAAGTGCACAACTGGCTGGTGTCCCGACCGAGATCGAGCGGGTGTGATCGCGCAC 10362

RESULT 8

US-08-474-933-1
; Sequence 1, Application US/08474933
; Patent No. 5866410
; GENERAL INFORMATION:
; APPLICANT: Ryan, Michael J.

APPLICANT: Lotvin, Jason A.
 APPLICANT: Strathy, Nancy
 APPLICANT: Fantini, Susan E.
 TITLE OF INVENTION: Cloning of the biosynthetic pathway for
 TITLE OF INVENTION: chlorotetracycline and tetracycline Formation and cosmid
 TITLE OF INVENTION: useful therein
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSER: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,933
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,468
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsevdos, Estelle J
 REGISTRATION NUMBER: 31,145
 REFERENCE/DOCKET NUMBER: 31,255-02.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201)831-3241
 TELEFAX: (201)831-3305
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30001 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 OS-08-474-933-1

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 118: em_estpl7:*
 119: em_estpl8:*
 120: em_estpl9:*
 121: em_estpl10:*
 122: em_estpl11:*
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 143: em_estpl32:*
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 181: em_estpl70:*
 182: em_estpl71:*
 183: em_estpl72:*
 184: em_estpl73:*
 185: em_estpl74:*
 186: em_estpl75:*
 187: em_estpl76:*
 188: em_estpl77:*
 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	549.8	22.5	582	8	AA539933	AA539933 LD19236.5
2	470.2	19.3	487	20	AI405401	AI405401 GH25390.5
3	148.2	6.1	569	18	AI293134	AI293134 GH18237.5
4	56.2	2.3	483	19	AI325858	AI325858 mf89d07.y
5	56.2	2.3	677	22	AI605559	AI605559 ma07h04.y
6	56.2	2.3	925	190	CNS0091P	AL053013 Drosophila
7	55.6	2.3	401	7	AA464375	AA464375 z81d11.r
8	55.6	2.3	925	190	CNS0091P	AL053013 Drosophila
9	54.6	2.2	318	147	W99136	W99136 mf89d07.r1
10	54.6	2.2	671	91	AW506290	AW506290 GE1674 G1
11	48.2	2.0	590	138	BE981482	BE981482 UI-M-CG0p
12	48.2	2.0	593	138	BE981393	BE981393 UI-M-CG0p
13	47.4	1.9	389	23	AI687362	AI687362 tp95a05.x
14	47.4	1.9	941	135	BE735881	BE735881 601305237
15	47.2	1.9	935	190	CNS0163Z	AL108265 Drosophila
16	46.2	1.9	1101	190	CNS0175Y	AL108460 Drosophila
17	45.2	1.8	1101	190	CNS0160E	AL107216 Drosophila
18	44.8	1.8	337	108	BE466893	BE466893 hz28d11.x
19	44.8	1.8	436	27	AI968607	AI968607 wt90e12.x
20	44.8	1.8	457	23	AI690321	AI690321 tz15g05.x
21	44.6	1.8	653	191	CNS02MID	AL203530 Tetraodon
22	44.4	1.8	908	190	CNS01678	AL108382 Drosophila
23	44.2	1.8	433	40	AW141778	AW141778 EST291867
24	44.2	1.8	839	190	CNS004NB	AL054280 Drosophila
25	43.8	1.8	586	111	BE680493	BE680493 df81b01.y
26	43.6	1.8	419	110	BE640340	BE640340 946084A02
27	43.6	1.8	1101	193	CNS05C4L	AL330654 Tetraodon
28	43.4	1.8	607	37	AV612885	AV612885 AV612885
29	43.4	1.8	632	93	AW644141	AW644141 cm37h06.w
30	43.2	1.8	368	24	AI739096	AI739096 w17h03.x
31	43.2	1.8	844	190	CNS0052P	AL056652 Drosophila
32	43.2	1.8	1124	191	CNS02Y0X	AL219930 Tetraodon
33	43.2	1.8	1008	191	CNS035YI	AL223347 Tetraodon
34	42.6	1.7	518	111	BE720244	BE720244 RCO-HT088
35	42.4	1.7	531	22	AI586911	AI586911 486057H11
36	42.4	1.7	594	20	AI444765	AI444765 486013C05
37	42.4	1.7	619	22	AI603727	AI603727 486082G10
38	42.2	1.7	369	5	AA308453	AA308453 EST179278
39	42.2	1.7	957	190	CNS015W7	AL105985 Drosophila
40	42.2	1.7	1011	192	CNS04LCX	AL295962 Tetraodon
41	42.2	1.7	237	25	AI804983	AI804983 tx03g04.x
42	42.2	1.7	417	140	C89710	C89710 C89710 Dict
43	41.8	1.7	380	97	AW952265	AW952265 EST364335
44	41.8	1.7	712	134	BE038709	BE038709 AB04D10.A
45	41.8	1.7	1039	191	CNS02ADN	AL188420 Tetraodon

ALIGNMENTS

RESULT 1
 AA539933
 LOCUS
 DEFINITION
 Drosophila melanogaster cDNA clone LD19236 5prime, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

AA539933 582 bp mRNA EST 27-NOV-1998
 LD19236.5prime LD Drosophila melanogaster embryo Bluescript
 Drosophila melanogaster cDNA clone LD19236 5prime, mRNA sequence.

AA539933.1 GI:2795149
 EST.
 fruit fly.


```
Db 241 CGGGGGCTCAGTCAATCTATTGGCGAACGACGCGGTCCGCCACCCCTTCGAAT 300
Qy 2011 cgaatgagcattggccagcggcgccgcttaacgaacatgggctccagatgag 2070
Db 301 CGAATGCGAGCTTGGCCAGCGCGCGGCTTAACGAACATGGGCTTCAGATGGAG 360
Qy 2071 atgagcaaccccgccatcgccattggcggtgagcctatcaacgaagcggtgctg 2130
Db 361 ATGAGCAACCCGCCATCGGCATTGGGGCGTGGAGCTATCAACGCAAGCGGCTGCTG 420
Qy 2131 gcaagcgcagcgcagagcatctacaccagaataacgcccatcgctcgccgggca 2190
Db 421 GCAGCGCCGACGCGAGAGCATCTACACCCAGAATCAAGCCCATCGCTCGCGGGGCA 480
Qy 2191 gcatgta 2197
Db 481 GCATGTA 487

RESULT 3
LOCUS AI293134 569 bp mRNA EST 01-DEC-1998
DEFINITION GH16237.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH16237 5prime, mRNA sequence.
ACCESSION AI293134
VERSION AI293134.1 GI:3942541
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 569)
AUTHORS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
P., Lewis,S. and Rubin,G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 162 row: D column: 1
High quality sequence stop: 515.
FEATURES
Source
1..569
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH16237"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
BASE COUNT 177 a 122 c 121 g 149 t
ORIGIN

Query Match 6.1%; Score 148.2; DB 18; Length 569;
Best Local Similarity 92.2%; Pred. No. 6.9e-29;
Matches 178; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy 1 acgcatccgcgcagtgatatttttttagcttcagtcttcagtggttcgcattct 60
Db 13 ACCGATCGCGGAGTGATATTTTTTTTAGCTCAGTCTTCAGTGTTCGCGATTCT 72
Qy 61 ctttaaaag-aaaaaataataagtcacaaactcaaacacacagcgaagcgcaaa 119
Db 73 CTTTAAAGAAAAAATAAATAAGTCAAAACTCAAAACACACAGCGGAAGCGGAAA 132
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Qy 120 g-caacgggttcctgcagtggtttatttttttttcaacaatttttgatogtagcgaca 178
Db 133 GCCAACGGTTCCTCGGAGTGTATTATTTTTCACAAATTTTTCATCGTGGTATCCT 192
Qy 179 atccgtcgagcat 191
Db 193 GAAAGTGAAGCAT 205

RESULT 4
LOCUS AI325858 483 bp mRNA EST 23-DEC-1998
DEFINITION m189d07.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:421453 5' similar to TR:035111 035111 MCTBAK. ; , mRNA
sequence.
ACCESSION AI325858
VERSION AI325858.1 GI:4060287
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 483)
AUTHORS Marta,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,C., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:256005
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 450.
FEATURES
source
1..483
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:421453"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 82 a 160 c 137 g 104 t
ORIGIN
```


[illegible]

RESULT	8
CNS0091P/c	
LOCUS	925 bp DNA
DEFINITION	Drosophila melanogaster genome survey sequence TER3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL053013
VERSION	AL053013.1 GI:4934461
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Artinropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 925)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a

please see <http://www.livulity.org> the BDPG *Drosophila* melanogaster BAC library was prepared by Kazuhiro Oosagawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial *NotI* digestion of *Drosophila* DNA provided by the BDPG from the isogenic strain y2; cn bw sp, the same strain used for the BDPG's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

```

FEATURES
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      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone_lib="RPC1-98"
      /clone="BACR19D16"
      /note="end : TET3"
BASE COUNT      120 a      61 c      61 g      172 t      511 others
ORIGIN
,
Query Match      2.3%; Score 55.6; DB 190; Length 925;
Best Local Similarity 12.3%; Pred. No. 0.00052;
Matches 43; Conservative 168; Mismatches 139; Indels 0; Gaps 0;

```


	Query Match	2.0%	Score 48;	DB 138;	Length 590;
	Best Local Similarity	56.2%;	Pred. No. 0.052;		
	Matches 90;	Conservative 0;	Mismatches 70;	Indels 0;	Gaps 0;
Qy	455	cgtggaacctctaccatgcctctcttcttcgcttcacggttgcctccacggtgggatatg	514		
Db	289	CTTGGAACTGGGAGCGCCCTCTTTTCTCGGGACCATCATCACTACCATCGGCTATG	230		
Qy	515	ggaatatatcgcaacacacttcggcgacggatgatcatgcgctattcggtgattg	574		
Db	229	GCATATAGTCTTACACACATGCGGGCGCTCTTTTGTATCTTCTATGCACCTGGTGG	170		
Qy	575	gcatacccgctcaatggtatctctctttgcccgcctcgcca	614		
Db	169	GGATCCCACTCTTCGGGATGCTGCTGGCGGAGTCGGGGA	130		

RESULT	12
BE981393/c	
LOCUS	BF981393
DEFINITION	UI-M-CG0p-bdb-f-11'-0-UI.s1 NIH-BMAP_Ret4_S2 Mus musculus cDNA clone.
	593 bp mRNA EST
	05-OCT-2000

EST. 014200004055
house musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 593)
Bonaldo,M.F., Lennon,G. and Soares M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Chin, H
National Institute of Mental Health
6001-Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mpe@emil.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence. Seq primer: M13 Forward
is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
POLYA-No.

```

I. 593
local/040411c1
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bdb-f-11-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/notes=Vector: pT713D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"
BASE COUNT      129 a      179 C      165 g      119 t      1 others
ORIGIN

Query Match      2.0%; Score 48; DB 138; Length 593;
Best Local Similarity 56.2%; Pred. No. 0.052;

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Db	145	AAAAATTTTAAAAAACCCCCCCCCCGGGGAAAAATAAAAAAAGCGCCCCCCCC	204
Qy	137	tgattttttttttt	153
Db	205	CTTTTttttttttttt	221
RESULT 14			
BE735881			
LOCUS	BE735881	941 bp	mRNA
DEFINITION	601305237F1 NIH_MGC_39	Homo sapiens	cDNA clone IMAGE:3639657 5', 15-SEP-2000 EST
ACCESSION	BE735881		mRNA sequence.
VERSION	BE735881.1	GI:10149873	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 941)		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Plate: LLCM342 row: j column: 10		
FEATURES	High quality sequence stop: 669.		
source	Location/Qualifiers		
	1. 941		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3639657"		
	/clone_lib="NIH_MGC_39"		
	/tissue_type="adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	112 a 292 c 344 g 193 t		
ORIGIN			
Query Match	1.98;	Score 47.4;	DB 135; Length 941;
Best Local Similarity	55.08;	Pred. No. 0.082;	
Matches	93; Conservative	0; Mismatches	76; Indels 0; Gaps 0;
Qy	446	cgccctacagtggaacctttacacatgcctctcttcgcttcacccgttttgcaccgg	505
Db	281	CGGACCCCGCTGGGACTTCGCCCTCTCTCTTCCTTCGCCAGCAGCTGATCACCACG	340
Qy	506	tgggatatgggaatatatcgcccaaccaccttcgcgcgcgcgatcatcatcgctatt	565
Db	341	TGGGCTATGGGTACACAAGGCATTGACTGATGCGGGCAGGCCCTTCTCCATCGCCTTG	400
Qy	566	cggtgatggcatccccogtcaatggatctcttgcgcgcgcctcgcgga	614
Db	401	CGCTCCTGGGCGTCCGACCAACCATGTGCTGCTGACCGCCTCAGCCCA	449

Search completed: March 17, 2001, 17:04:13
Job time: 4286 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2001, 18:53:13 ; Search time 77.65 Seconds
(without alignments)
272.141 Million cell updates/sec

Title: US-08-816-011C-2

Perfect score: 3283

Sequence: 1 MSPNRWILLIPYSLMFG.....DAVRHPSNRMAWPAAG 618

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 3413795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_36.*
- 1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
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 - 3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3283	100.0	618	17 R97984	DmORF1 potassium c
2	301.5	9.2	398	20 Y30647	A mechanically sen
3	301	9.2	499	21 Y94875	Human protein clon
4	298.5	9.1	370	20 Y30648	A mechanically sen
5	298.5	9.1	411	20 Y28497	Mouse h-TREK1 poly
6	292.5	8.9	411	20 Y34133	Human potassium ch
7	292.5	8.9	411	20 Y28496	h-TREK1 polypeptid
8	286	8.7	393	21 Y94425	Human h-TRAAK poly
9	286	8.7	393	21 Y94426	Human h-TRAAK poly
10	239	7.3	336	18 W23397	h-TREK1 potassium c
11	231.5	7.1	394	21 Y87291	Human signal pepti
12	210.5	6.4	313	20 Y34132	Human potassium ch

13	210.5	6.4	313	20 Y25116	Human hTREK-1 prot
14	210.5	6.4	313	21 Y68737	KT4, a TWIK family
15	210.5	6.4	313	21 Y68738	KT5, a TWIK family
16	204.5	6.2	336	17 R97986	P22b7.7 potassium
17	169.5	5.2	107	20 Y28498	Partial h-TREK1 po
18	116.5	3.5	888	20 Y17399	Human erg subfamil
19	114	3.5	824	20 Y24001	A potassium channel
20	114	3.5	962	21 Y83032	Rat Bag1 potassium
21	110.5	3.4	2019	16 R67913	Cardiac sodium cha
22	110.5	3.4	2466	16 R71498	Human protein tyro
23	110.5	3.4	2466	19 W75999	Intracellular prot
24	110	3.4	2270	16 R69604	Calcium channel al
25	109	3.3	1081	20 Y13443	Amino acid sequenc
26	109	3.3	1105	20 Y13442	Amino acid sequenc
27	109	3.3	2251	16 R71009	Human neuronal cal
28	109	3.3	2270	16 R71010	Human neuronal cal
29	107.5	3.3	383	19 W98461	H. pylori GPO 718
30	105.5	3.2	408	18 W20814	H. pylori cell env
31	102	3.1	962	21 Y49944	Human potassium io
32	102	3.1	989	21 Y49945	Human potassium io
33	101.5	3.1	354	19 W74521	Human ATP-sensitiv
34	101.5	3.1	364	19 W74518	Human ATP-sensitiv
35	101.5	3.1	390	18 W13103	Mouse ATP sensitiv
36	101.5	3.1	390	18 W17932	Human K-ATP channel
37	101.5	3.1	390	18 W17931	Mouse K-ATP channel
38	101.5	3.1	390	19 W74516	Mouse ATP-sensitiv
39	101.5	3.1	390	19 W74517	Human ATP-sensitiv
40	101	3.1	655	19 W75990	Human Kv potassium
41	100.5	3.1	390	18 W13102	Human ATP sensitiv
42	98.5	3.0	160	20 Y32009	Streptomyces livid
43	98.5	3.0	2020	11 R06584	Cardiac sodium cha
44	97.5	3.0	570	21 Y57377	Human KVLQT1 prote
45	97.5	3.0	581	18 W33355	Human KVLQT1 assoc

ALIGNMENTS

RESULT	1
R97984	
ID	R97984 standard; Protein; 618 AA.
XX	
AC	R97984;
XX	
DT	16-OCT-1996 (first entry)
XX	
DE	DmORF1 potassium channel protein.
XX	
KW	DmORF1; potassium channel; fruitfly; pore-forming domain;
KW	transmembrane helix; N-glycosylation site; potassium-agonist;
KW	potassium-antagonist; drug screening; insecticide; cardiac disorder.
XX	
OS	Drosophila melanogaster.
XX	
FH	Key
FT	Domain
FT	Location/Qualifiers
FT	6..27
FT	/note= "Transmembrane domain M1"
FT	Modified-site
FT	58..60
FT	/note= "N-glycosylation site"
FT	95..111
FT	Domain
FT	/note= "Pore-forming domain H5-1"
FT	120..140
FT	Domain
FT	/note= "Transmembrane domain M2"
FT	171..191
FT	Domain
FT	/note= "Transmembrane domain M3"
FT	208..224
FT	Domain
FT	/note= "Pore-forming domain H5-2"
FT	242..263
FT	Domain
FT	/note= "Transmembrane domain M4"
XX	
PN	W09613520-AL.
XX	
PD	09-MAY-1996.

Db 7 lallalvlylvsalvgaleqheqqaqkmdhgrdqfirdhpcvsgksledfiklilv 66
QY 52 BELGKNTTQDEILQRIIDYCDKPVTLPTVDDTPYTWTFVHAFEFATVGVGNI 111
Db 67 ealgg-----anpetswnssnhssawngsafggtiittigygni 110
QY 112 SPTFAGRMIMTAYSVIGIPVNGILFAGLGEVFGRT-----FEALYRKYKYMSTDM 164
Db 111 vhtdagrlfcfayalvgplfmgllagvgrdlgsrlrgighlealfkw----- 161
QY 165 HVPVQLGLITVWIALPGIALFLVPCVGVHLLRELGLSISLYSVYVTTTIGFGDY 224
Db 162 -hvpvgvlrsisavlligellvltptf-vfsmeswskleayfvltttvgfgy 219
QY 225 VFTGANQKPEGWFVYQIVFVIFVIFSLGYLVIMTFTIRGLQS-----KKLAYLE 278
Db 220 vvgdgtgqnsq-----ayqplvfwilfayfasvlttignwlravrrtraemggit 273
QY 279 QOLSSNLKATQRIWSG-----VTKDVG 301
Db 274 aqaas-----wtgtvtarvtrdtg 292

RESULT 3
Y94875
ID Y94875 standard; Protein; 499 AA.
AC Y94875;
XX
DT 12-JUN-2000 (first entry)
XX
DE Human protein clone HP10538.
XX
KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;
KW cytokine production; cell proliferation; cell differentiation;
KW immune deficiency; infectious disease; autoimmune disorder; asthma;
KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
KW coagulation disorder; myocardial infarction; inflammatory condition;
KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
KW nephritis; therapy.
XX
OS Homo sapiens.
XX
PN WO200005367-A2.
XX
PD 03-FEB-2000.
XX
PF 22-JUL-1999; 99WO-JP03929.
XX
PR 24-JUL-1998; 98JP-0208820.
PR 07-AUG-1998; 98JP-0224105.
PR 25-AUG-1998; 98JP-0239116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
PA (SAGA) SACAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2000-182694/16.
XX
PT Novel human proteins having hydrophobic domains useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
PS Claim 1; Page 245-247; 351pp; English.
XX
CC This sequence represents a human protein of the invention, which has

CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also acts as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
SQ Sequence 499 AA;

Query Match 9.2%; Score 301; DB 21; Length 499;
Best Local Similarity 24.6%; Pred. No. 2.6e-22;
Matches, 133; Conservative 93; Mismatches 227; Indels 88; Gaps 23;

QY 4 NWILLIFYSYLMFGAALYHIEHGEKISRADQKQAIINEYLLLEELGDKNTTOD 63
Db 3 drgplltsaifylaigaafvelephwk-----eaknyttqkhlhkefclgqegid 58

QY 64 EILQRIIDYCDKPVTLPTVDDTPYTWTFVHAFEFATVGVGNIPTFAGRMIMI 123
Db 59 kilevvsdaagdvai--tgnqtfnnwnpnamifaatvittigynvapkpapgrfvcv 116

QY 124 AYSVICIPVNGILFAGLGEYFGRTFEALYRKYKYMSTDMHYVPPQLGLITVWIALIP 183
Db 117 fygflgvplcltwisalgkffg-----grakrlgqfltkrgvsirkaqitctvfiwv 169

QY 184 GIALFLVPCVGVHLLRELGLSSI-SLYSVYVTTTIGFGDYVPTFGANQKPEFGWFV 242
Db 170 gvlvhlvipff-vfmvte-gwnyieglyysfistigfgdva--gvnps---anyhal 222

QY 243 YOIFVIVWFIFSLGYLVIMTFT-----ITRGLQSKLAYLEQQLSS--NLKATONRIW 293
Db 223 yryfvelwiylglawlsifvnkwsmfvevhkaikrrrrrkesfessphskalqv-k 281

QY 294 SGVTKDVGYLRRMLNELYLKVKPVVTDV--DIAYTL-----PRSNSCP 335
Db 282 staskdvnifs-----flskkeetyndlikqgkkmktsgggetgpgpglpgqggp 335

QY 336 DLSMRVVEPAPISKRRAFSVCADWVGQREAGWVHANSOTDLTKLDRKKTETAYHQ 395
Db 336 alppslv-plvysknrv-ptleevsqtirskghvsrpsdeavapadesspapevfmm 393

QY 396 TTDLLAKVVALATVKPPPAEOEDAAALGYGKG--FSDSQILASEWSFSFVNFTSPRRP 453
Db 394 qlidrise-----ecepwdagq-----yhlplfqdasitfvnteaglsdeets---- 435

Db	106	ivaainagiaplgnssnqvshwdlgssffagtvittlgtfgnisprteggkfcilayall	165
Qy	129	GIPVNGILFAG----LGEYGRFTFEALYRRYKKYKMSDMMHYVPPOLGLITTVIALIPG	184
Db	166	gipifgflagvgdqgtifgkgiakvedtfikwnvs-----qtkiriistiifilf-g	218
Qy	185	IALFLVLPCVGVHLLREL-GLSSI-SLYYSYVTTTTTIGFGDYVPTFGANQPKFEGGMFVV	242
Db	219	cvlifaipav---ifkhiegwsaldalyfvvittltitlgfdgya-----ggsdle	265
Qy	243	YOIRV--IVWF--IFSGLYLVMTMTFITRGLQ--SKKLAYLEQQLSSNLKATONRIWSGV	296
Db	266	yltdykpvvfwilvglayfaavlsmigdlwlrisk-----tkeevgefrahaewtany	321
Qy	297	TKDGYLRLMLN-ELY 311	
Db	322	taefketrrrlsveyi 337	
RESULT	5		
Y28497			
ID	Y28497	standard; Protein; 411 AA.	
XX	AC	Y28497;	
XX	DT	12-OCT-1999 (first entry)	
XX	DE	Mouse h-TREK1 polypeptide.	
XX	KW	h-TREK1; two pore potassium channel; inflammatory disease;	
XX	KW	chromosome 1q32.	
OS	XX	Mus musculus.	
PN	XX	W09937762-A1.	
PD	XX	29-JUL-1999.	
PF	XX	02-DEC-1998; 98WO-EP07805.	
XX	XX	09-OCT-1998; 98GB-0022135.	
PR	XX	27-JAN-1998; 98EP-0300570.	
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.	
PI	XX	Chapman CG, Meadows HJ;	
XX	XX	WPI; 1999-469126/39.	
DR	XX	N-PSDB; Z00040.	
PT	XX	New two pore potassium channel used for, e.g. treatment of cancer,	
PT	XX	pulmonary, cardiovascular and inflammatory diseases	
PS	XX	Claim 3; Page 26; 44pp; English.	
XX	XX	This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1	
XX	CC	polynucleotide Z00040. h-TREK1 is a two pore potassium channel.	
CC	CC	The polynucleotide sequence of h-TREK1 can be used to diagnose a	
CC	CC	disease or susceptibility to a disease related to expression or activ	
CC	CC	of h-TREK-1 polypeptides. The methods of diagnosis may be used in the	
CC	CC	treatment of diseases including cancer, pulmonary, cardiovascular, an	
CC	CC	inflammatory diseases, pain, psychiatric disorders including depressi	
CC	CC	and schizophrenia, neurodegenerative diseases including Alzheimer's,	
CC	CC	stroke, and head trauma and neurological disorders including migraine	
XX	XX	Sequence 411 AA;	
SQL			
Query Match		9.1%; Score 298.5; DB 20; Length 411;	
Best Local Similarity		28.5%; Pred. No. 3.5e-22;	
Matches	90; Conservative	64; Mismatches 121; Indels 41; Gaps	
QY	9	LLIFYISYLMFGAAIYHHIEHGEEKISRAEORKAQIAINEYLLLEELGDKNTTODEILOR	68

Db 50 iflvvlyliigaavfkalepqq-----isqrttviqkqfiaghaacvnsteldeliqq 105
Qy 69 ISDYCDKVPVTLPTPTVDDPTPTWTFYHAFFFAFVTCSTVGYGNISPTTFAGRMIMLAYSVI 128
Db 106 iaaainagiaplgnssnqshwdlgssffagvtlttfgnisprrteggkfcilayali 165
Qy 129 GIPVNGILFAG-----LGEYFGRTFEAIYRRYKMYKMSDMMHYVPPQLGLITTVVIALIPG 184
Db 166 gipifgllagvgdqlgtifgkgiakvedtfikwnvs-----qtkiriistifiilf-g 218
Qy 185 IALFLVPCVGVHLLREL-GLSSI-SLYSYVTTTIGFGDVPTTFGANQPKFEGGWV 242
Db 219 cvlfvalpav-----ifkhiegwsaldailyfvvltlttfgdyva-----ggsdie 265
Qy 243 YQIFV--IVWF--IFSLGYLVNMTFTRGLQ--SKKLAYLEQQLSSNLKATQNRWISGV 296
Db 266 yldfykpvvfwilvlayfaavlsimgdwlrvlsk-----tkeevgefrahaetaanv 321
Qy 297 TKDVGYLRRMLN-ELY 311
Db 322 taefketrirrsvely 337

RESULT 6
Y34133 standard; Protein; 411 AA.
XX AC Y34133;
XX DT 30-NOV-1999 (first entry)
XX DE Human potassium channel K+Hnov59.
XX KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
XX KW cardiovascular disorder; CNS disorder; renal disorder.
XX OS Homo sapiens.
XX PN WO9943696-A1.
XX PD 02-SEP-1999.
XX PF 22-FEB-1999; 99WO-US03826.
XX PR 19-JAN-1999; 99US-0116448.
XX PR 25-FEB-1998; 98US-0076687.
XX PR 07-AUG-1998; 98US-0095836.
XX FA (AXYS-) AXYS PHARM INC.
PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;
XX WPI: 1999-527591/44.
XX DR N-FSDB; Z11915.

New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
Claim 3; Page 104-105; 112pp; English.

This sequence represents the human K+Hnov59 potassium channel. K+Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is located on chromosome 19, determined via PCR chromosomal localisation using primers Z11939 and Z11940. K+Hnov cDNAs were isolated by extension of expressed sequence tags (ESTs) which were related but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple independent clones. Potassium channels have critical roles in various

cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all cells, it is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) disorders. Nucleotides encoding K+Hnov proteins may be used for identifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hnov protein in fermentation cultures. Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.

XX SQ Sequence 411 AA;

Query Match 8.9%; Score 292.5; DB 20; Length 411;
Best Local Similarity 25.2%; Pred. No. 1.5e-21;
Matches 108; Conservative 72; Mismatches 153; Indels 95; Gaps 18;

Qy 9 LLIFVISYLMFGAIIYHIEHGEERKISRAEQRKAOIAINEXLLEELGDKNTTQDEILQR 68
Db 50 iflvvlyliigaavfkalepqq-----isqrttviqkqfiaghaacvnsteldeliqq 105
Qy 69 ISDYCDKVPVTLPTPTVDDPTPTWTFYHAFFFAFVTCSTVGYGNISPTTFAGRMIMLAYSVI 128
Db 106 iaaainagiaplgnssnqshwdlgssffagvtlttfgnisprrteggkfcilayali 165
Qy 129 GIPVNGILFAG-----LGEYFGRTFEAIYRRYKMYKMSDMMHYVPPQLGLITTVVIALIPG 184
Db 166 gipifgllagvgdqlgtifgkgiakvedtfikwnvs-----qtkiriistifiilf-g 218
Qy 185 IALFLVPCVGVHLLREL-GLSSI-SLYSYVTTTIGFGDVPTTFGANQPKFEGGWV 242
Db 219 cvlfvalpai-----ifkhiegwsaldailyfvvltlttfgdyva-----ggsdie 265
Qy 243 YQIFV--IVWF--IFSLGYLVNMTFTRGLQ--SKKLAYLEQQLSSNLKATQNRWISGV 296
Db 266 yldfykpvvfwilvlayfaavlsimgdwlrvlsk-----tkeevgefrahaetaanv 321
Qy 297 TKDVGYLRRMLNELYLKVKPVYTDVDTATYLPNSNCPDLSMYRVEPAPISRRKAFSV 356
Db 322 taefketrirrs-----velydkfqratsl-----krkls- 351
Qy 357 CADMVGAOREAGMVHANSDTLTLDREKTFFETAEAYHOTTDLLAKVVNALATVKKPPAE 416
Db 352 -aelag-----nhnqeltpprr-----tlsvnhltse-----rdvippllk 386
Qy 417 QEDAALYG 424
Db 387 tesiyng 394
RESULT 7
Y28496
ID Y28496 standard; Protein; 411 AA.
XX AC Y28496;
XX DT 12-OCT-1999 (first entry)
XX DE h-TREK1 polypeptide.
XX KW h-TREK1; two pore potassium channel; inflammatory disease;
XX KW chromosome 1q32.
XX OS Homo sapiens.
XX PN WO9937762-A1.
XX PD 29-JUL-1999.

QY 288 TONRIWSG-----VTKDVG 301
Db 278 -----wtgtvtarvtqrag 291

RESULT 9
Y94426
ID Y94426 standard; Protein: 393 AA.
AC Y94426;
XX
XX 04-AUG-2000 (first entry)
DE Human h-TRAAK polypeptide #2.
XX
XX Human; h-TRAAK: potassium channel polypeptide;
KW 2P domain potassium channel; neurodegenerative disease; stroke;
KW psychiatric disorder; neurological disorder; Gene therapy.
XX
XX Homo sapiens.
PN WO200026253-A1.
XX
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-GB03634.
XX
XX 03-NOV-1998; 98GB-0024048.
PR
XX 07-OCT-1999; 99GB-0023668.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Chapman CG, Duckworth DM;
XX
XX WPI: 2000-365583/31.
DR N-PSDB: A27106.
XX
XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel
PT family of polypeptides, useful for the diagnosis and treatment of
PT h-TRAAK related disorders, e.g. depression and schizophrenia
XX
XX Claim 12; Pages 21 and 22; 35pp; English.
XX
XX Functional genomics was used to identify h-TRAAK polypeptides and
CC h-TRAAK polynucleotides from human tissue samples. h-TRAAK
CC polypeptides have homology to the 2P domain potassium channel family of
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may
CC be used in diagnostic assays for conditions related to h-TRAAK
CC imbalance and for identifying agonists and antagonists of h-TRAAK
CC polypeptides. The h-TRAAK polypeptides and polynucleotides may also
CC be useful for treatment and prevention (e.g. as vaccines) of certain
CC diseases, such as pain, psychiatric disorders including depression and
CC schizophrenia, neurodegenerative disease including Alzheimer's, stroke
CC and head trauma and neurological disorders including migraine and
CC epilepsy. The present sequence is human h-TRAAK protein #2.
XX
XX Sequence 393 AA;
SQ

Query Match 8.7%; Score 286; DB 21; Length 393;
Best Local Similarity 27.9%; Pred. No. 6.4e-21;
Matches 89; Conservative 57; Mismatches 115; Indels 58; Gaps 11;

QY 7 ILLLFYISYLMFGAAIYHIEHGEEKISRFAQKRAQIAINEYLLEELGDKNTTQDEIL 66
Db 7 lallalvilyvsqalvraleqph-----qqdqreigevrekflrahpcvsdqelg 59
QY 67 QRISYCD-----KPVTLPTPTDPTWTFYHAFFFFAFTVCSVGYGNISPTTFAGRM 120
Db 60 llikevadalgaggadpet-nstsnsshsawldgsaffsgtiittigynvalrtdagrl 118
QY 121 IMIAYSVTIGIPVNGILFAGLGEYFGRT-----FEAYIRRYKKYKMTDMHYVPPQLGL 173

Db 119 fcifyalvgipfllagvgdrgissrhghighieaiflk-----hvppeivr 168
QY 174 ITVVIALIPGIALFLVLPVPCVHLLRELGLSSISLYSYVTTTIGFGDVPTFGANOP 233
Db 169 vlsmflilicllflvtptf-vfcymedwskleaiyfviutlttvgfdyva--gadpr 225
QY 234 KEFGWFVVYQIFVIVWFIFSLGYLVIMTITRGLQ-----SKKLAYLEQQLSSNLKA 287
Db 226 qd-----spayqplvwfllglayfasvlttignwlrvsvrrtraemggltaqaas---- 277
QY 288 TONRIWSG-----VTKDVG 301
Db 278 -----wtgtvtarvtqrag 291

RESULT 10
W23397
ID W23397 standard; Protein: 336 AA.
XX
XX W23397;
XX
XX 17-MAR-1998 (first entry)
DE TWIK-1 potassium channel protein.
XX
XX TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
KW Tandem of P domains in a Weak Inward rectifying K⁺; antibody.
XX
XX Homo sapiens.
XX
XX FR2744730-A1.
XX
XX 14-AUG-1997.
XX
XX 08-FEB-1996; 96FR-0001565.
XX
XX 08-FEB-1996; 96FR-0001565.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;
PI Lesage F, Romey G;
XX
XX WPI: 1997-427773/40.
DR N-PSDB: T64960.
XX
XX Nucleic acid encoding new potassium channel designated TWIK-1 -
PT useful for treating channel deficiency diseases, screening for
PT active agents and for diagnosis
XX
XX Claim 12; Figure 1b; 37pp; French.
XX
XX The present sequence represents a protein comprising a potassium channel
CC with the properties of a TWIK (Tandem of P domains in a weak inward
CC rectifying K⁺)-1 channel. This is the first member of a new family of
CC channels consisting of 4 transmembrane segments and two P domains, and
CC being only weakly rectifying. The cDNA, vectors, the cells expressing
CC TWIK-1 type channels and the protein are used to compensate
CC for deficiency of potassium channels in various tissues. Compounds
CC for modulating activity of TWIK-1 type channels may also be useful
CC therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
CC disease, neurodegeneration (particularly of ischemic or anoxic origin),
CC endocrine or muscular disorders. The cDNA and the vectors can also be
CC used to create transgenic animals (especially knock-out animals) for use
CC as models of TWIK-1 related diseases. Analysis of the sequence of the
CC TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
CC can be used to detect TWIK-1 channels and for inhibiting or activating
CC the channels in vivo.
XX
XX Sequence 336 AA;
SQ

```
Query Match 7.3%; Score 239; DB 18; Length 336;
Best Local Similarity 28.1%; Pred. No. 3.7e-16;
Matches 74; Conservative 49; Mismatches 112; Indels 28; Gaps 8;

QY 9 LLIFYSYLMFGAAIYVHIEGEEKISRQRQAQIAINEYLLLELGDKNNTTQDEILQR 68
DB 26 lvigyllylgavvsvsvelpyedllrqlrk----lkrflleehclseqqlqglgr 81
QY 69 ISDYCDKPVTLPPYDDPTWTFYHAFFAFTVCSYGVGNISPTTFAGRMIMIAYSVI 128
DB 82 vleasnvgvsvlnasgn-wnwdfstalfastvltstgthvtpisdgkafciylsvi 140
QY 129 GIPVNGILFAGLGEYFQRTFAYRYRYKYMSTDMHYVPPQLGL---ITVWVIALPG- 184
DB 141 gipft-llf-----ltavvqrithvtrpvllyfhrwgfskqvvaivhavllgf 189
QY 185 --TALFLVLCVGHLLRELGLSSISLYSYVTITTTIGFGDYVPTFCANQPKFEGHFV 242
DB 190 vtscffifpaavsvldedwnflesfycflstglstglgdyvpgyngdk-----frel 244
QY 243 YQIFVIVWFISL-GYLVIMIMTF 264
DB 245 ykigitcylllgliamlvletf 267

RESULT 11
Y87291
XX Y87291 standard; Protein; 394 AA.
AC Y87291;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-68 SEQ ID NO:68.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neuroprotection; neuroprotection; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
XX WO200000610-A2.
XX
PD 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1998; 98US-0090762.
XX 31-JUL-1998; 98US-0094983.
XX 01-OCT-1998; 98US-0102686.
XX 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akribiom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
XX N-PSDB; 298176.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease
XX
XX Claim 1; Page 207-208; 327pp; English.
XX
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CC 298109 to 298242 encode y87224 to y87357 which represent the human
CC signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neuroprotection, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor,
CC HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 394 AA;
```

```
Query Match 7.1%; Score 231.5; DB 21; Length 394;
Best Local Similarity 23.1%; Pred. No. 2.9e-15;
Matches 94; Conservative 76; Mismatches 150; Indels 87; Gaps 16;

QY 5 RWLLLIYFISYLMFGAAIYVHIEGEEKIS-----RQPKQAQIAINEYLLLELGDKN 58
DB 7 rtialivctfyllvgaavfdalesepelierrlelrgqlrarnysggvyeel---- 62
QY 59 TTTQDEILRISDYCDKPVTLPPYDDPTWTFYHAFFAFTVCSYGVGNISPTTFAG 118
DB 63 -----ervlrl-----kp-----hkagvqwrfgsfyfaivtittigvghaapstdgg 106
QY 119 RMTIMAYSIVIGIPVNGILFAGLGEYFQRTFAYRYRYKYMSTDMHYVPPQLGL----I 174
DB 107 kvfcmyallgpltlvmfsglgerintivrylhrakk-----gigmrradv 154
QY 175 TTVVIALPGIALFLVLCVGHLLR--ELGLSSISLYSYVTITTTIGFGDYVPTFCANO 232
DB 155 smanmvliffscistl-cigaaafshyehwtffqyyycfittigtigdyv-alqkdq 212
QY 233 PKFEGGFVYVYQIFVIVWFISLGYL--VMIMTFITRGLQSKKLAYLEQOL----- 281
DB 213 alqtqpyvafsfvyltltvlgafnlvrlfvtmnaedekrdehrralltrngagq 272
QY 282 -----SSNLKATQNRNLSGVTKDGYLRRLNEL-YILKVPYVTDVDTAYTL 328
DB 273 gggggsahttdtasstaaagggrfnvyaevlhfgmcsclywksreklqys---ipmli 329
QY 329 PRNSNCPDLNMYRVEAP-----IPSKRAFSVCADMVGAQREA 367
DB 330 prdlstsdctveqshspgggrysdtparr---clcs---gaprsa 370

RESULT 12
Y34132
XX Y34132 standard; Protein; 313 AA.
XX
AC Y34132;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K-Hnov49.
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder.
XX
```



```
XX SQ Sequence 313 AA;
Query Match 6.4%; Score 210.5; DB 20; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;
QY 10 LIFVISLMEGAAYIHIEHGEKISRAEQKQAIAINEYLLLELGDKNKTTTODEILQRI 69
DB 11 laayaaylvigallvarleghearlae-----le-----tlraqllqr- 50
QY 70 SDYCDKPVTLPPTYD-----DTPYTWTFYHAFFAFTVCS 104
DB 51 -----spcvaapaldafervlaagrlgrvvlanasgsanaspawdfasalfastlit 105
QY 105 TVGYGNISPTTFAGRMIMAYSIGIPVNGILFAGLGEYFGRTEFYAIRYKRYKMDSTM 164
DB 106 tvgygytptldagkafsaifallgvpttmllltasaqrlsllthvplswlsmrgwdp 165
QY 165 H-----YVPPQLGLITVVIALLIPGIALFLVPCVGHLLRELGLSSISLYSVVTTTII 219
DB 166 rraacwhlvallgvvtv-----cfilvpavifah-leeawsfldafyfcfislsti 215
QY 220 GFQGYVPTFGANQPKFGGWFVYQIFVIVWFIFSLGYLVMM-TF 264
DB 216 glgdyvpgaeagqp-----yralkylvltvylfglvamvltqtf 256
RESULT 14
Y68737
ID Y68737 standard; Protein; 313 AA.
AC Y68737;
XX
XX 05-MAY-2000 (first entry)
XX
XX KT4, a TWIK family 2PD potassium channel polypeptide.
XX
XX KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
XX expressed sequence tag; EST; AA604914; ion channel dysfunction;
XX renal disease; musculoskeletal disease; proliferative disease;
XX renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
XX muscular dystrophy; atherosclerosis; cancer.
XX
XX Homo sapiens.
XX
XX WO200003687-A2.
XX
XX 27-JAN-2000.
XX
XX 20-JUL-1999; 99WO-US16471.
XX
XX 20-JUL-1998; 98US-0093486.
XX
XX 13-AUG-1998; 98US-0096655.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Forsayeth JR, Zhao BB, Chavez RA;
XX
XX WPI; 2000-171196/15.
XX
XX N-PSDB; 246092.
XX
XX Novel human potassium channel polynucleotides and polypeptides used in
XX the diagnosis, prevention and treatment of diseases including renal
XX failure, cirrhosis, muscular dystrophy and cancers -
XX
XX Claim 4; Fig 1A-C; 53pp; English.
XX
XX The present sequence represents a protein, designated KT4, which is a
XX member of the TWIK family 2PD potassium channel polypeptides. These
XX polypeptides contain two potential P-domains and 8 (preferably 4)
XX transmembrane domains. The KT4 cDNA sequence was isolated from a brain
```

```
CC cDNA library using degenerate oligonucleotides derived from human
CC expressed sequence tag (EST) AA604914. The polypeptides and
CC polynucleotides are used in the diagnosis, prevention and treatment of
CC disease states. The polynucleotides may be used to detect and
CC quantitate expression of TWIK family 2PD potassium channels, and
CC aberrant or mutant forms of the polynucleotide which cause various
CC diseases and disorders. Antisense oligonucleotides may be used to
CC modulate the expression of polynucleotides of the invention. The
CC polypeptides are used for treating diseases and disorders associated
CC with ion channel dysfunction, including renal, musculoskeletal and
CC proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
XX and cancers.
XX
XX Sequence 313 AA;
SQ
Query Match 6.4%; Score 210.5; DB 21; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;
QY 10 LIFVISLMEGAAYIHIEHGEKISRAEQKQAIAINEYLLLELGDKNKTTTODEILQRI 69
DB 11 laayaaylvigallvarleghearlae-----le-----tlraqllqr- 50
QY 70 SDYCDKPVTLPPTYD-----DTPYTWTFYHAFFAFTVCS 104
DB 51 -----spcvaapaldafervlaagrlgrvvlanasgsanaspawdfasalfastlit 105
QY 105 TVGYGNISPTTFAGRMIMAYSIGIPVNGILFAGLGEYFGRTEFYAIRYKRYKMDSTM 164
DB 106 tvgygytptldagkafsaifallgvpttmllltasaqrlsllthvplswlsmrgwdp 165
QY 165 H-----YVPPQLGLITVVIALLIPGIALFLVPCVGHLLRELGLSSISLYSVVTTTII 219
DB 166 rraacwhlvallgvvtv-----cfilvpavifah-leeawsfldafyfcfislsti 215
QY 220 GFQGYVPTFGANQPKFGGWFVYQIFVIVWFIFSLGYLVMM-TF 264
DB 216 glgdyvpgaeagqp-----yralkylvltvylfglvamvltqtf 256
RESULT 15
Y68738
ID Y68738 standard; Protein; 313 AA.
AC Y68738;
XX
XX 05-MAY-2000 (first entry)
XX
XX KT5, a TWIK family 2PD potassium channel polypeptide.
XX
XX KT5; TWIK family 2PD potassium channel polypeptide; P-domain;
XX expressed sequence tag; EST; AA533124; ion channel dysfunction;
XX renal disease; musculoskeletal disease; proliferative disease;
XX renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
XX muscular dystrophy; atherosclerosis; cancer.
XX
XX Homo sapiens.
XX
XX WO200003687-A2.
XX
XX 27-JAN-2000.
XX
XX 20-JUL-1999; 99WO-US16471.
XX
XX 20-JUL-1998; 98US-0093486.
XX
XX 13-AUG-1998; 98US-0096655.
XX
XX (ELAN-) ELAN PHARM INC.
XX
XX Forsayeth JR, Zhao BB, Chavez RA;
XX
XX
```

```
DR WPI: 2000-171196/15.
DR N-PSDB: 246094.
XX
PT Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -
XX
PS Claim 7; Fig 3A-C; 53pp; English.
XX
CC The present sequence represents a protein, designated KT5, which is a
CC member of the TWIK family 2PD potassium channel polypeptides. These
CC polypeptides contain two potential P-domains and 8 (preferably 4)
CC transmembrane domains. The KT4 cDNA sequence was isolated from a brain
CC cDNA library using degenerate oligonucleotides derived from human
CC expressed sequence tag (EST) AA533124. The polypeptides and
CC polynucleotides are used in the diagnosis, prevention and treatment of
CC disease states. The polynucleotides may be used to detect and
CC quantitate expression of TWIK family 2PD potassium channels, and
CC aberrant or mutant forms of the polynucleotide which cause various
CC diseases and disorders. Antisense oligonucleotides may be used to
CC modulate the expression of polynucleotides of the invention. The
CC polypeptides are used for treating diseases and disorders associated
CC with ion channel dysfunction, including renal, musculoskeletal and
CC proliferative diseases, e.g. renal failure, nephrosis, cirrhosis,
CC dysphagia, gastritis, myotonias, muscular dystrophy, atherosclerosis
CC and cancers.
XX
SQ Sequence 313 AA;

Query Match 6.4%; Score 210.5; DB 21; Length 313;
Best Local Similarity 24.5%; Pred. No. 3e-13;
Matches 70; Conservative 42; Mismatches 103; Indels 71; Gaps 9;

Qy 10 LIFYSYLMFGAAIYHYEHGEKISRAEQKQAIANEYLLEELGDKNTTQDEILORI 69
Db | | :||: || : :| | ||| | | : :|||
Qy 70 SDYCDKPVTLPTYP-----DTPYTWTFYHAFFFAFTVCS 104
Db | | :||: || : :| | ||| | | : :|||
Qy 105 TVGYNISPTTFAGRMIMAYSVIGIPVNGILFAGLGEYFGFTFEAIRRYKKYKXMTDM 164
Db ||||| :| | | :| :||: || : :| | : :|
Qy 165 H-----YVPPOLGLTTVVIALPGIALFLVLPVGVHLLRELGLSSLSLYSVYVTTTI 219
Db | | :||: || : :| | ||| | | : :|||
Qy 220 GFGDYVPTFGANQPKFEGGVFVYQIFVIMVFIISGLYLVIMIM-TF 264
Db | | |||| | | : :||: || : :| | : :|||
Qy 216 glgdyvpgeapqp-----yralykvltvylflglvamvvlvlttf 256
Db | | |||| | | : :||: || : :| | : :|||
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Search completed: March 17, 2001, 19:57:18
Job time: 3845 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 19:24:58 ; Search time 65.58 Seconds
(without alignments)
169.220 Million cell updates/sec

Title: US-08-816-011C-2

Perfect score: 3283

Sequence: 1 MSPNRWILLIFYISYLMFG.....DAVRHPSNRMAAPAAAG 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6-COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3283	100.0	618	1	US-08-332-312-2
2	239	7.3	336	3	Sequence 2, Appli
3	204.5	6.2	336	1	Sequence 2, Appli
4	189	5.8	383	3	Sequence 4, Appli
5	165.5	5.0	347	3	Sequence 3, Appli
6	116.5	3.5	888	2	Sequence 4, Appli
7	116.5	3.5	888	2	Sequence 4, Appli
8	110.5	3.4	2465	2	Sequence 3, Appli
9	110.5	3.4	2465	3	Sequence 3, Appli
10	110.5	3.4	2466	3	Sequence 12, Appli
11	110.5	3.4	2466	4	Sequence 12, Appli
12	101.5	3.1	390	2	PCT-US94-09943-2
13	100.5	3.1	390	2	US-08-614-156B-3
14	100	3.0	1754	1	US-08-614-156B-1
15	100	3.0	1754	1	US-07-745-206A-13
16	97.5	3.0	581	3	US-08-311-363-13
17	97.5	3.0	676	3	US-09-135-021-80
18	93.5	2.8	434	3	US-08-135-021-2
19	93	2.8	770	1	US-08-725-459B-42
20	92	2.8	3169	2	US-08-445-135-2
21	89	2.7	1159	2	US-08-477-451-6
22	89	2.7	1159	2	US-08-956-242-13
23	88.5	2.7	626	3	US-09-351-215-13
24	88.5	2.7	626	3	US-08-956-242-2
25	88.5	2.7	1481	2	US-09-351-215-2
26	88.5	2.7	1481	2	US-08-616-844-40
27	88.5	2.7	1481	2	US-08-599-654-40
28	88.5	2.7	1481	3	US-08-944-868A-40
					US-08-944-423A-40

29 88.5 2.7 1481 3 US-08-944-496-40 Sequence 40, Appli
30 88.5 2.7 2289 3 US-09-051-019-2 Sequence 2, Appli
31 88 2.7 369 2 US-08-424-224-2 Sequence 2, Appli
32 88 2.7 369 4 PCT-US94-02891-69 Sequence 69, Appli
33 87.5 2.7 1503 3 US-08-976-255-14 Sequence 14, Appli
34 86.5 2.6 424 2 US-08-614-155B-1 Sequence 1, Appli
35 86.5 2.6 424 2 US-08-614-155B-3 Sequence 3, Appli
36 86.5 2.6 532 1 US-08-288-405A-10 Sequence 10, Appli
37 86.5 2.6 557 1 US-08-424-788-6 Sequence 6, Appli
38 86.5 2.6 578 1 US-08-424-788-5 Sequence 5, Appli
39 86.5 2.6 578 1 US-08-110-683-2 Sequence 2, Appli
40 86.5 2.6 578 2 US-08-683-743-2 Sequence 2, Appli
41 86.5 2.6 578 2 US-08-472-166-2 Sequence 2, Appli
42 86.5 2.6 578 2 US-08-472-097-2 Sequence 2, Appli
43 86.5 2.6 578 4 PCT-US93-11638-2 Sequence 2, Appli
44 86.5 2.6 1969 3 US-08-836-325-16 Sequence 16, Appli
45 86 2.6 902 1 US-08-396-479B-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-332-312-2

; Sequence 2, Application US/08332312

; Patent No. 5559026

; GENERAL INFORMATION:

; APPLICANT: Price, Laura A.

; APPLICANT: Pausch, Mark H.

; TITLE OF INVENTION: Functional Expression of a Drosophila

; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESS: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: US

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/332.312

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Harrington, James J.

; REGISTRATION NUMBER: P-38,711

; REFERENCE/DOCKET NUMBER: 32,421

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3246

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 618 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-332-312-2

Query Match 100.0%; Score 3283; DB 1; Length 618;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSPNRWILLIFYISYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT 60

|||||

Db 1 MSPNRWILLIFYISYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT 60

|||||

Oy 61 TDEILQRISDYCDKPVTLPTTYDDTPTWTFTYHFAFFAFTVCSTVGXGNISPTTFAGRM 120

```
Db 61 TQELQRIQSDYCKPVTLPPTDPTTWTYHAEFFAFVTCSTVGYNISPTTFAGRM 120
QY 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEALYRKYKMSMDHYVPPQGLITTVVIA 180
Db 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEALYRKYKMSMDHYVPPQGLITTVVIA 180
QY 181 LIPGIALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWF 240
Db 181 LIPGIALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWF 240
QY 241 VYQIFVIVWFIFSLGYLWIMFIFTRGLOSLLAYLEQQLSSNLKATQNRINSGVTKDV 300
Db 241 VYQIFVIVWFIFSLGYLWIMFIFTRGLOSLLAYLEQQLSSNLKATQNRINSGVTKDV 300
QY 301 GYLRLMNELYLKVRPVYTDVIAVTLPRNSCPDLSMYRVEPAPIPSRKRAFSVCADM 360
Db 301 GYLRLMNELYLKVRPVYTDVIAVTLPRNSCPDLSMYRVEPAPIPSRKRAFSVCADM 360
QY 361 VQAQREAGMVFHANSDDTLTKLDREKTFETAEYHQTDDLLAKVYNALATVKPPPAEQEDA 420
Db 361 VQAQREAGMVFHANSDDTLTKLDREKTFETAEYHQTDDLLAKVYNALATVKPPPAEQEDA 420
QY 421 ALYGGYHGFSDSILASEWSFVNEFTSPRRPRARACSDFNLEAPRWQSERPLRSRSHNE 480
Db 421 ALYGGYHGFSDSILASEWSFVNEFTSPRRPRARACSDFNLEAPRWQSERPLRSRSHNE 480
QY 481 WTWSGDNQIQEAFNORYKQQRANGAANSTWVHLPEALDEEOLRNHRVPVARSPPCR 540
Db 481 WTWSGDNQIQEAFNORYKQQRANGAANSTWVHLPEALDEEOLRNHRVPVARSPPCR 540
QY 541 MVDVCFPSRRSPRRIRWSASCPSWRSRYPRVSSRRKPDPRWTTTSTRSRPPVNPICATDA 600
Db 541 MVDVCFPSRRSPRRIRWSASCPSWRSRYPRVSSRRKPDPRWTTTSTRSRPPVNPICATDA 600
QY 601 VRURPSNRMAWPAAG 618
Db 601 VRURPSNRMAWPAAG 618

RESULT 2
US-08-749-816-2
; Sequence 2, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemate, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
```

```
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989,6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-816-2

Query Match 7.3%; Score 239; DB 3; Length 336;
Best Local Similarity 28.1%; Pred. No. 8.7e-17;
Matches 74; Conservative 49; Mismatches 112; Indels 28; Gaps 8;

QY 9 LLIFFIYSLMFGAAIYYHIEHGEKISRAEQRKAQIAINEYLLLEELGDKNNTTQDEILQR 68
Db 26 LVLGYLLLVFCAVFSVSELPYEDLLRQELRK----LKRFFLEEHECLSEQOLEQFLGR 81
QY 69 ISDYCDKPVTLPTPTDPTTWTYHAEFFAFVTCSTVGYNISPTTFAGRMIMIAYSVI 128
Db 82 VLEASNYGVSVLSNASGN-WNMDFTSALFFASTVLTSTGYGTVPLSDGGKAFCAIYSVI 140
QY 129 GIPVNGILFAGLGEYFGRTFEALYRKYKMSMDHYVPPQGL---ITTVVIALIPG- 184
Db 141 GIPFT-LLF-----LTAVQRTVHVRPRVLYFHIRMGFSKQVVAIVHAVLLGF 189
QY 185 --IALFLVPCGVHLLRELGLSSISLYSVVTTTIGFGDYVPTFGANQKKEGGWFV 242
Db 190 VIVSCFFIPAAVSVLEDDWNFLESFYCFISLSIGLDYVPGEGYNOK-----FREL 244
QY 243 YQIFVIVWFIFSL-GYLVIMTF 264
Db 245 YKIGITCYLLGLLIAMLVVLETF 267

RESULT 3
US-08-332-312-4
; Sequence 4, Application US/08332312
; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Functional Expression of a Drosophila
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
```



```

; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Welser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989,6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-3

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Query Match 5.0%; Score 165.5; DB 3; Length 347;
Best Local Similarity 25.0%; Pred. No. 5.5e-09;
Matches 78; Conservative 38; Mismatches 109; Indels 87; Gaps 12;

Qy	1	MSPN-----RWILLIFYSYLMF---GAAYIYHHGEHGEKTSRAFPORQAIAINE 48
Db	22	MSPTNRQFRQNVVNVVSAATLLVFNLIAGIFY-----LAETQNSSESLE 71
Qy	49	YLLEELGDKNTTODEILORISYCDKPVTLPTTYDDTPVTWTFYHAFFFAFTVCSTVG 108
Db	72	NSEVSKLHNLPIGGKTAEMKSKLCKCLTKSRIDG-----FGKAIFFSWTLTYSTVG 125
Qy	109	GNISPTTFAGRMIMAYSVIGIIPVNGILFAGLGEYFG-----RTPEAIYRRYK 156
Db	126	GSYPHSTLGRYLTIFYSLMIPV---FIAKFEEGTFLAHFLVVSNNRTRLAVKKAY 181
Qy	157	KYKMSDMMHVVPQ-----LGLITTVVIALIGIALFLVLPVCGVHLLRELGLSSI 207
Db	182	KLSONPENAETPSNSLQHDYLIFLSLLLCSSISLLSSSALFSSNI SY-----LSSV 234
Qy	208	SLYYSVTTTTIGFDYVPTFGANQPKFGGWFVVQIFVWVFIISGLYVNIWTFITR 267
Db	235	--YFGIITMFLIGIDIVPT-----NLVWF-----SGY---CMFLIS 267
Qy	268	GLQSKKLAYLEQ 279
Db	268	DVLSNOIFYFCO 279

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RESULT      6
US-08-956-242-4
; Sequence 4, Application US/08956242C
; Patent No. 5986081
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/08/956,242C
; CURRENT FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (133)
; OTHER INFORMATION: Unidentified at time of filing
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (181)
; OTHER INFORMATION: Unidentified at time of filing

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FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing.
LOCATION: (438)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (439)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (567)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (568)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (575)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (571)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (580)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (589)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (593)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (599)	
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LOCATION: (600)	
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LOCATION: (621)	
OTHER INFORMATION:	
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NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (624)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (625)	
OTHER INFORMATION:	
FEATURE:	
NAME/KEY: unsure	Unidentified at time of filing
LOCATION: (628)	
OTHER INFORMATION:	
FEATURE:	

Best Local Similarity 20.3%; Pred. No. 0.095;
Matches 66; Conservative 52; Mismatches 118; Indels 89; Gaps 13;
QY 263 TPTIRGLQSKKLAYLEQQLSSNLKATQNRINSGVTKDVGYYLRRLMLNE----- 309
DB 231 TFLNKGKLSKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSENTFCP 274
QY 310 -----LYTLKVKPVY-TDVIDIAYTLPRNSCPDLSMYR-----VEPA 345
DB 275 YQFTSGGPEKKPIPIGIDVLSSKKIWAASMDLLCTADRFSSGETATYRCHPEAVTVRTS 334
QY 346 PIPSRKRA-----FSVCADMVGAQREAGVMVHANSQDITLTKLDREKTFETAAYHQTDLILA 401
DB 335 TTPRKKEARYSDGSIALDIFGPKMDPIYHT-----RELPTSSAISALDRIR 382
QY 402 KVVNALATVKKPPAQEDAAALGGYHG--FSDS-----QILASEWSFSTVNEFTSPRRPRA 455
DB 383 ERQKKLQVLRAMNVEEPVRYKTYHGDVFSTSSPSISSE-----SDPRQVRRSEA 436
QY 456 RACSFENLEAP-----RWQSERPLRSHNWTWSGDNQOIQEAFNORYKQOORANGAA 508
DB 437 SKRFESSGLPGVDITLQSGOSQSRPSQYETPFEGNLINEIMLRQEEELMOLQAKMAL 496
QY 509 NSTMVHLEP-DALEQLRNNHRVPV 532
DB 497 ROSRLSLYPGDTIKASMLDITRDPL 521
RESULT 9
US-09-100-804-3
; Sequence 3, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAFSSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100.804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: L0461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-804-3
Query Match 3.4%; Score 110.5; DB 3; Length 2465;
Best Local Similarity 20.3%; Pred. No. 0.095;
Matches 66; Conservative 52; Mismatches 118; Indels 89; Gaps 13;
QY 263 TPTIRGLQSKKLAYLEQQLSSNLKATQNRINSGVTKDVGYYLRRLMLNE----- 309
DB 231 TFLNKGKLSKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSENTFCP 274
QY 310 -----LYTLKVKPVY-TDVIDIAYTLPRNSCPDLSMYR-----VEPA 345
DB 275 YQFTSGGPEKKPIPIGIDVLSSKKIWAASMDLLCTADRFSSGETATYRCHPEAVTVRTS 334
QY 346 PIPSRKRA-----FSVCADMVGAQREAGVMVHANSQDITLTKLDREKTFETAAYHQTDLILA 401
DB 335 TTPRKKEARYSDGSIALDIFGPKMDPIYHT-----RELPTSSAISALDRIR 382
QY 402 KVVNALATVKKPPAQEDAAALGGYHG--FSDS-----QILASEWSFSTVNEFTSPRRPRA 455
DB 383 ERQKKLQVLRAMNVEEPVRYKTYHGDVFSTSSPSISSE-----SDPRQVRRSEA 436
QY 456 RACSFENLEAP-----RWQSERPLRSHNWTWSGDNQOIQEAFNORYKQOORANGAA 508
DB 437 SKRFESSGLPGVDITLQSGOSQSRPSQYETPFEGNLINEIMLRQEEELMOLQAKMAL 496
QY 509 NSTMVHLEP-DALEQLRNNHRVPV 532
DB 497 ROSRLSLYPGDTIKASMLDITRDPL 521
RESULT 10
US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franzen, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gopez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080.855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12
Query Match 3.4%; Score 110.5; DB 3; Length 2466;
Best Local Similarity 20.3%; Pred. No. 0.095;
Matches 66; Conservative 52; Mismatches 118; Indels 89; Gaps 13;
QY 263 TPTIRGLQSKKLAYLEQQLSSNLKATQNRINSGVTKDVGYYLRRLMLNE----- 309
DB 231 TFLNKGKLSKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSENTFCP 274
QY 310 -----LYTLKVKPVY-TDVIDIAYTLPRNSCPDLSMYR-----VEPA 345

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Db 231 TFLNKL-SKSMGFL-----SIKDTQ-----DENYFKDILSDNSGREDSENTFSP 274
Qy 310 -----LYLVKVPVY-TDVIATYTLPRNSCPDLSMYR-----VEPA 345
Db 275 YQKFTSGPEKKPIPGIDVLSSKKIWAASSMDLLCTADRFSSGETATYRRCRHPAENVTRTS 334
Qy 346 PIPSRKRA----FVSCADMYGAQREAGWVHANSDDTLTKLDREKTFETAAYHQTTDLLA 401
Db 335 TTPRKKEARYSDGSIALDIFGPKQMDPIYHT-----RELPTSATSSAALDRIR 382
Qy 402 KVMNALATVPPPAEQEADALYGYHG--FSDS-----QILASEWSFSTVNEFTSPRRPA 455
Db 383 EROKKLOVLRAMNVEPVRYKTYHGVFSTSESPSIISSE-----SDFQVRSE 436
Qy 456 RACSDFNLEAP-----RWQSRPLRSSHNWETWSDGNOQIOEAFNQRKYKGOORANGAA 508
Db 437 SKRFESSGUGVDETLSSQGSQSRPSROYETTPFEGNLINQEIIMLKQEEELMLOAKMAL 496
Qy 509 NSTWVHLEP-DALEEOLRNHRVPV 532
Db 497 QRSRLSLPGDTIKASMLDITRDPL 521

RESULT 12
US-08-614-156B-3
; Sequence 3, Application US/08614156B
; Patent No. 5917027
; GENERAL INFORMATION:
; APPLICANT: Susumu SEINO et al.
; TITLE OF INVENTION: NOVEL ATP-SENSITIVE POTASSIUM-CHANNEL
; TITLE OF INVENTION: PROTEINS AND THEIR GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,156B
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 264943/1995
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10890/P60282US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-638-6666
; TELEFAX: 202-393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-614-156B-3

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Query Match 3.1%; Score 101.5; DB 2; Length 390;
Best Local Similarity 26.3%; Pred. No. 0.039;
Matches 45; Conservative 27; Mismatches 56; Indels 43; Gaps 7;
QY 91 TFYHAFFFAFTGCTGCGNISPTTFAGM-----IMIAYSVIGIPVNGILFAGL 140

Db 116 SFSSAFLEIEVQVITGFG-----GRMTEECPLAILIVONIVGLMINAIM---L 164
Qy 141 GEYGRTEAAYRYKKYKMSMDHYVPPQLGITVVIALLPGIALFLVLPVCGVHLLR 200
Db 165 GCIEFMKTAQA-HRRAETLIFSKH-----AVITLRHGRLCFM---LRVGDRL 206
Qy 201 ELGLSSISLYSYVTTTIGFDYVPTFGANQPKFEG-----GWFFVYQIFV 247
Db 207 KSMIISATIHQVVRKTTSPGEVVPPLHQVDIPMENGVGNGIPLVAPLII 257

RESULT 13

US-08-614-156B-1
; Sequence 1, Application US/08614156B
; Patent No. 5917027
; GENERAL INFORMATION:
; APPLICANT: Susumu SEINO et al.
; TITLE OF INVENTION: NOVEL ATP-SENSITIVE POTASSIUM-CHANNEL
; TITLE OF INVENTION: PROTEINS AND THEIR GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,156B
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 264943/1995
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10890/P60282USQ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-638-6666
; TELEFAX: 202-393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-614-156B-1

Query Match 3.1%; Score 100.5; DB 2; Length 390;
Best Local Similarity 26.8%; Pred. No. 0.05;
Matches 42; Conservative 25; Mismatches 51; Indels 39; Gaps 6;

Qy 91 TFYHAFFAFTVCSYGVGNISPTTFAGRMI-----MIAYSIVIGIPVNGILFAGL 140
Db 116 SFSSAFLEIEVQVITGFG-----GRMTEECPLAILIVONIVGLMINAIM---L 164
Qy 141 GEYGRTEAAYRYKKYKMSMDHYVPPQLGITVVIALLPGIALFLVLPVCGVHLLR 200
Db 165 GCIEFMKTAQA-HRRAETLIFSKH-----AVITLRHGRLCFM---LRVGDRL 206
Qy 201 ELGLSSISLYSYVTTTIGFDYVPTFGANQPKFEG 237
Db 207 KSMIISATIHQVVRKTTSPGEVVPPLHQVDIPMENG 243

RESULT 14

US-07-745-206A-13
; Sequence 13, Application US/07745206A
; Patent No. 5429921
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 135 S. LaSalle
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/745,206A
; FILING DATE: 19910815
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B
; REFERENCE/DOCKET NUMBER: 51504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-745-206A-13

Query Match 3.0%; Score 100; DB 1; Length 1754;
Best Local Similarity 21.2%; Pred. No. 0.69;
Matches 121; Conservative 69; Mismatches 184; Indels 196; Gaps 34;

Qy 120 MIMTAYSIGIPVNGILFAG-----LGEYFG---RTFEAYRYRKYKYM 160
Db 1276 LFMFTFAVIAVQ---LFGKFFYCTDESKELERDCRQYLDYEKEVEEAQPROWKY-- 1329
Qy 161 STDHMYVPPQLGITVVIALLPGIALFLVLPVCGVHLLRELGLSSISLYSYVTTTIG 220
Db 1330 --DFHYDNVWALLFTVTSTGEG-----WPMVLKH-----SVDATYE----- 1365
Qy 221 FGDDYPTFGANQPKFEGFWVYQIFVIVWFIF--SLGYLVMIIMTIFTRG-----LQS 271
Db 1366 --EQGPSGGRM--ELSIFFVYVY--FVVPPFFVNFVIALIIITFQEGDKVMSCSLEK 1419
Qy 272 KKLAYLEQQLSS-----NLKATQNRISGVTKDGYLRMLNELYLKLVKPVYTDV 322
Db 1420 NERACIDFAISAKPLTRYMPQNRQSFQKWTFFVVSPP-----FEYFIMAMIALNTVV 1472
Qy 323 -----DIAYTLPRNSCPDL---SMYRVEPAPIPSRKRAFSVCADMVGAQREAGMVHAN 373
Db 1473 LMKFYDAPYEYELMLKCLNIVFTSMFSME-----CVLKITA---FGVLNYF 1516
Qy 374 SDTDLTKLDREKTFETAEAYHOTDULLAKVNVNALTATVKKPPPAEQEDAAALYGYHGFSDSQ 433
Db 1517 RDA-----WNFVDFVTVLGSITDILVTEI-----AICPRRFQOCYCTPG----- 1557
Qy 434 ILASEWSFSTVNEFT-----SPRRPRARACS-DFNLEAPRQWSEPLRS----- 476

Db 1558 -----VTVTLTHQORRICPVSHSPRSPLSLESASKEPPLVSPVFGSERVIOQFTGI 1609
QY 477 --SHNEWTSGDNOQIOEA-FNORYKQQRANGAANSTVHLEPDALAEOLRNHRPVVA 533
Db 1610 TVSRNSWKRTISTSSASSASFELR-----GSSCSARATPSA-----SCCGPLS 1652
QY 534 SRSSPC-RMVC DV-CFPRSRTSPRIWSASC-----PWSRYPRVSSRRKPDPRWTTTST 585
Db 1653 SPSRPCPTCVCSLPCCSS--STP-----SSACRCLGILPWNMTTASTA-----TTTSG 1698
QY 586 RSRPPVPNPICATDAVHRPSNRMAAPAA 615
Db 1699 RF-----CKPCCCGAPRGPRGTR-SCCPAA 1723

RESULT 15

US-08-311-363-13
; Sequence 13, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1754 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-363-13

Query Match 3.0%; Score 100; DB 2; Length 1754;
Best Local Similarity 21.2%; Pred. No. 0.69;
Matches 121; Conservative 69; Mismatches 184; Indels 196; Gaps 34;
QY 120 MIMAYSVIGIPVNGILFAG-----LGEYFG---RTEEAIVRYKKYKM 160
Db 1276 LWFIFAVIAVQ-----LFKGEFFYDESKELERDCRGQILDYEKEVEAQPQWKY--- 1329
QY 161 STDHMYVPPQLGITTVIALIPGIALFLVPCVGVHLLRELGLSSISLSYVTTTIG 220

Db 1330 --DFHYDNVLMALLTLTFTVSTGEG-----WPMVLKH-----SVDATYE----- 1365
QY 221 FGDYVTFEGANQPKFCGWFVVYQIEVIVWFIF-SLGYLVIMTFTIRG-----LOS 271
Db 1366 --EQGSPSPGYRM--ELSIFFVYV--FWVTFVFNIFVALIITITFOEGDKVMSECSLEK 1419
QY 272 KKLAYLEQQLSS-----NLKATQNRISGVTKDVGYLRRMLNELYLKVKPVVTDV 322
Db 1420 NERACIDFAISAKPLTRYMPQNQSFQYKWTWTFVVSPP-----FEYFIMAMIALNTVV 1472
QY 323 -----DIAYTLPRNSCPDL-----SMYRVEPAPIPSRKRAFSCVADWVGQAQRAGMVHAN 373
Db 1473 LMKFYDAPYEYELMLKCLNIVFTSMFME-----CVLKIIA---FGVLNYF 1516
QY 374 SDTDLTKLDREKTFETAAYHQTTDLLAKVVNALATVKKPPPAEQEDAALYGGYHGSDSQ 433
Db 1517 RDA-----WNEVDFVTVLGSDITDILVTEI-----AICPRRFQFCYSTPG----- 1557
QY 434 ILASENSFSTVNEFT-----SPRRPRARACS-DENLEAPRWOSERPLRS----- 476
Db 1558 -----VTVTLTHQORRICPVSHSPRSPLSLESASKEPPLVSPVFGSERVIOQFTGI 1609
QY 477 --SHNEWTSGDNOQIOEA-FNORYKQQRANGAANSTVHLEPDALAEOLRNHRPVVA 533
Db 1610 TVSRNSWKRTISTSSASSASFELR-----GSSCSARATPSA-----SCCGPLS 1652
QY 534 SRSSPC-RMVC DV-CFPRSRTSPRIWSASC-----PWSRYPRVSSRRKPDPRWTTTST 585
Db 1653 SPSRPCPTCVCSLPCCSS--STP-----SSACRCLGILPWNMTTASTA-----TTTSG 1698
QY 586 RSRPPVPNPICATDAVHRPSNRMAAPAA 615
Db 1699 RF-----CKPCCCGAPRGPRGTR-SCCPAA 1723

Search completed: March 17, 2001, 19:58:38
Job time: 2020 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 19:25:53 ; Search time 69.96 Seconds
(without alignments)
599.809 Million cell updates/sec

Title: us-08-816-011c-2
Perfect score: 3283
Sequence: 1 MSPNRWILLIIFYISYLMFG.....DAVRHRPSNRMAWPAAG 618
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.66:*
1: Pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2652	80.8	1001	2 T13807	potassium channel
2	264.5	8.1	551	2 T16436	hypothetical prote
3	264.5	8.1	555	2 T43357	potassium channel
4	264	8.0	393	2 T25392	hypothetical prote
5	247	7.5	523	2 T23373	hypothetical prote
6	242	7.4	452	2 T21118	hypothetical prote
7	239	7.3	336	2 S65566	inward rectifier p
8	238.5	7.3	364	2 T43361	probable potassium
9	233.5	7.1	329	2 T43509	probable potassium
10	233	7.1	334	2 T19860	hypothetical prote
11	232	7.1	485	2 T24201	hypothetical prote
12	231	7.0	336	2 T32347	outward rectifier
13	229.5	7.0	631	2 T26232	hypothetical prote
14	229	7.0	461	2 T43394	potassium channel
15	227.5	6.9	528	2 T21834	hypothetical prote
16	223.5	6.8	325	2 T15584	hypothetical prote
17	223	6.8	513	2 T28933	hypothetical prote
18	222.5	6.8	586	2 T21683	hypothetical prote
19	220.5	6.7	504	2 T22269	hypothetical prote
20	220.5	6.7	539	2 T23700	hypothetical prote
21	217.5	6.6	643	2 T26616	hypothetical prote
22	216	6.6	1136	2 T26953	hypothetical prote
23	215	6.5	335	2 S44635	f22b7.7 protein -
24	211.5	6.4	484	2 T43529	probable potassium
25	211.5	6.4	519	2 T16629	hypothetical prote
26	210	6.4	522	2 T24265	hypothetical prote
27	204.5	6.2	475	2 T27725	hypothetical prote
28	203	6.2	1539	2 T30037	hypothetical prote
29	201.5	6.1	392	2 T45032	hypothetical prote

RESULT 1
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from D
A:Reference number: Z17770; MUID:97075152
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <GOL>
A:Cross-references: EMBL.U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1
C:Genetics:
A:Gene: ORK1
A:Map position: 1

Query Match 80.8%; Score 2652; DB 2; Length 1001;
Best Local Similarity 90.9%; Pred. No. 1.3e-205;
Matches 518; Conservative 10; Mismatches 32; Indels 10; Gaps 4;

Qy 1 MSPNRWILLIIFYISYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT 60
Db 1 MSPNRWILLIIFYISYLMFGAAIYVHIEGEEKISRAEORAKQAIANEYLLLELGDKNNT 60
Qy 61 TQDEILQRISDYCDKPVTLPPYDDTPYTWTFYHAFFAFTVCSYVGNISPTTFAGRM 120
Db 61 TQDEILQRISDYCDKPVTLPPYDDTPYTWTFYHAFFAFTVCSYVGNISPTTFAGRM 120
Qy 121 IMIAYSVTIGIPVNGILFAGLGEYFGRTFAIYRKYKMYKMSDMMHYVPPQLGITVIVA 180
Db 121 IMIAYSVTIGIPVNGILFAGLGEYFGRTFAIYRKYKMYKMSDMMHYVPPQLGITVIVA 180
Qy 181 LIPGALFLVPCVGHLLRELGLSSISLYSYVTTTIGFDYVPTFGANPKFEGWF 240
Db 181 LIPGALFELLPS-WVFYFENWPYSISLYSYVTTTIGFDYVPTFGANPKFEGWF 239
Qy 241 VVYQIFVIWVFIISGLYLVIMTFITRGLQSKKLAYLEQQLSSNLKATONRISWGVTKDV 300
Db 240 VVYQIFVIWVFIISGLYLVIMTFITRGLQSKKLAYLEQQLSSNLKATONRISWGVTKDV 299
Qy 301 GYLRLMLNELYLKVKPVYTDVDIATLPRNSCPDLSMYRVEPAPIPSRKRAFSVCA 360
Db 300 GYLRLMLNELYLKVKPVYTDVDIATLPRNSCPDLSMYRVEPAPIPSRKRAFSVCA 359
Qy 361 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYHOTTDLLAKVNALATVKKPPPAQEDA 420
Db 360 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYROTTDLLAKVNALATVKKPPPAQEDA 419

ALIGNMENTS

QY 421 ALYGGYHGFSDSOLASEWSEFSTVNEFTSPRRPRARACSDNFLEAPRWQSERPLRSSHNE 480
Db 420 ALYGGYHGFSDSOLASEWSEFSTVNEFTSPRRPRARACSDNFLEAPRWQSERPLRSSHNE 479
QY 481 WTSGDGNQIQEAFNORYKQQRANGAANSTMVHLEPDALAEELNNHRRVPAVSRSRSPCR 540
Db 480 WTSGDGNQIQEAFNORYKQQRANGAANSTMVHLEPDALAEELNNHRRVPAVSRSRSPCR 537
QY 541 MCVDDV-CFPPSRSTP-----RRWSASCP 563
Db 538 MPDGLRLFPFKRRSQDLERKLSVSVSP 567

RESULT 2
T16426
hypothetical protein F52E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16426
R:Martin, J.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid F52E4.
A:Reference number: Z16512
A:Accession: T16426
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-551 <MAR>
A:Cross-references: EMBL:U56964; NID:g1293826; PID:g2078439; PIDN:AAB54033.1; GSPDB:GNOC
A:Experimental source: strain Bristol N2; clone F52E4
C:Genetics:
A:Gene: CESP.F52E4.4
A:Map position: x
A:Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

Query Match 8.1%; Score 264.5; DB 2; Length 551;
Best Local Similarity 23.3%; Pred. No. 2.3e-13;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

QY 9 LLIFYISYLMFGAAIYYHIE---HGEEKISRABQRAQIAINEYLLEEL--GDKNTTOD 63
Db 25 LLMVLVLYSFLGFGIFDRIETNAHAEMKNERINRTACVS---QILHSIHRWHSNTHKV 81
QY 64 EILQISDYCDKPVTLPPYDDPTTYTFYHAFFFAFTVSTVGYGNISPTTFAGRMIMI 123
Db 82 QVAEDIAD-CFEP-----EKDERSEWNFVTATLYGFGIVTTLGYNRIAPITVYGRMFCI 134
QY 124 AYSVIGIPVNGILFAGLGEYFG-----RTPEAIYRYKK-----YKMSDMMHY 166
Db 135 VYGICGIPVTMIILANVGQYLNNAFAGDSRRKIEA-YRQORMSKASLACKIYKES----- 189
QY 167 VPPQLGLITTVIALIPGIALFLVPCVGVHLL-----RELGLSSISLYSYVTTTIGFG 222
Db 190 -----IQVTSIAL---LCVFLIYVAVGALLPLNGELDFEN-GLYFNFLCLTAIDFG 238
QY 223 DYVPTGANOPKEFGWVYQIFVIVWFISGLYLVMIWTFITRGLQSKKLAYLEQQLS 282
Db 239 QLVF-----IRVELLPITFLYVCGIGLAITTIATINIGSEYMKKLHYWGCKMK 284
QY 283 SNLKATONRIWSGVTKDVGYLRLMELYLKVKPVYTDVDTAYTLPRNSCPDLSMYRV 342
Db 285 N---AAQTRIFWGGK-----TLKVR-----DLLHAV--GKKC-----GV 313
QY 343 EPAPISRRKRAFSVCADMVGAOREAGMVHANSDDLTKLDREKTFETABAYHOTDOLLA 402
Db 314 EP-----GMIDA---LDLENV-VERTIAMOEGREPPEDLNDE 346
QY 403 VVNALATVPPPAEQDAALYGGYHGFSDSOLASEWSEFSTVNEFTSPRRPRARACSDNF 462
Db 347 -----PPREP-----SPRSIIHSPCSTRPSNPPMSPSPREDHPFIK 384
QY 463 LEAPRWQSERPL-----RSSHNEWTSGDNOQIOE-AFNQRYKGOORAN----- 505

Db 385 MDAPAPRSPLPLPAYELDKKKPIFQALSNEFM-----NQAQEKLFNDLDTFQIEINTELV 440
QY 506 -GAANSTMVHLEPDALAEELNNHRRVPAVSRSRSPCR-----TPRR 556
Db 441 EDHKESVIIIEPPATFEDMTIOHSLCVDYEREKVPKR-----FREKKEMYGRDPRK 494
QY 557 IWSA-SCPWSRYPRVSRRRKPPDRPTTTSTRSRPPVNPICATDAVRH 603
Db 495 LYETQIEWDRLERLSD-RKHGPRKRSVLNLSNCSPEVS-SPSPIRH 540

RESULT 3
T43357
potassium channel chain n2p16 homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43357
R:Wang, Z.W.; Kunkel, M.T.; Wei, A.; Butler, A.; Salkoff, L.
Ann. N. Y. Acad. Sci. 868, 286-303, 1999
A:Title: Genomic organization of nematode 4TM K⁺ channels.
A:Reference number: Z22446; MUID:99342707
A:Accession: T43357
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-555 <MAN>
A:Cross-references: EMBL:AF083645; PIDN:AAC32856.1

Query Match 8.1%; Score 264.5; DB 2; Length 555;
Best Local Similarity 23.3%; Pred. No. 2.3e-13;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

QY 9 LLIFYISYLMFGAAIYYHIE---HGEEKISRABQRAQIAINEYLLEEL--GDKNTTOD 63
Db 29 LLMVLVLYSFLGFGIFDRIETNAHAEMKNERINRTACVS---QILHSIHRWHSNTHKV 85
QY 64 EILQISDYCDKPVTLPPYDDPTTYTFYHAFFFAFTVSTVGYGNISPTTFAGRMIMI 123
Db 86 QVAEDIAD-CFEP-----EKDERSEWNFVTATLYGFGIVTTLGYNRIAPITVYGRMFCI 138
QY 124 AYSVIGIPVNGILFAGLGEYFG-----RTPEAIYRYKK-----YKMSDMMHY 166
Db 139 VYGICGIPVTMIILANVGQYLNNAFAGDSRRKIEA-YRQORMSKASLACKIYKES----- 193
QY 167 VPPQLGLITTVIALIPGIALFLVPCVGVHLL-----RELGLSSISLYSYVTTTIGFG 222
Db 194 -----IQVTSIAL---LCVFLIYVAVGALLPLNGELDFEN-GLYFNFLCLTAIDFG 242
QY 223 DYVPTGANOPKEFGWVYQIFVIVWFISGLYLVMIWTFITRGLQSKKLAYLEQQLS 282
Db 243 QLVF-----IRVELLPITFLYVCGIGLAITTIATINIGSEYMKKLHYWGCKMK 288
QY 283 SNLKATONRIWSGVTKDVGYLRLMELYLKVKPVYTDVDTAYTLPRNSCPDLSMYRV 342
Db 289 N---AAQTRIFWGGK-----TLKVR-----DLLHAV--GKKC-----GV 317
QY 343 EPAPISRRKRAFSVCADMVGAOREAGMVHANSDDLTKLDREKTFETABAYHOTDOLLA 402
Db 318 EP-----GMIDA---LDLENV-VERTIAMOEGREPPEDLNDE 350
QY 403 VVNALATVPPPAEQDAALYGGYHGFSDSOLASEWSEFSTVNEFTSPRRPRARACSDNF 462
Db 351 -----PPREP-----SPRSIIHSPCSTRPSNPPMSPSPREDHPFIK 388
QY 463 LEAPRWQSERPL-----RSSHNEWTSGDNOQIOE-AFNQRYKGOORAN----- 505
Db 389 MDAPAPRSPLPLPAYELDKKKPIFQALSNEFM-----NQAQEKLFNDLDTFQIEINTELV 444
QY 506 -GAANSTMVHLEPDALAEELNNHRRVPAVSRSRSPCR-----TPRR 556
Db 445 EDHKESVIIIEPPATFEDMTIOHSLCVDYEREKVPKR-----FREKKEMYGRDPRK 498
QY 557 IWSA-SCPWSRYPRVSRRRKPPDRPTTTSTRSRPPVNPICATDAVRH 603


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Query Match 7.1%; Score 233.5; DB 2; Length 329;
Best Local Similarity 26.8%; Pred. No. 3.6e-11;
Matches 79; Conservative 47; Mismatches 96; Indels 73; Gaps 11;

QY 5 RWILLIFVISLMEFGAIIYHIEGEEKISRAEORAKQAIANEYLLELGGKNTTQDE 64
DB 7 RTLSLIVCTLTLLVGAADFALFENEIL-----ORKLVORREKLTKYKNSN----- 56

QY 65 ILQISDYCDKVPPLPTTY-DPTPTWTFYHAFFAFTVCSVGVGNISPTTFAGRMIMI 123
DB 57 -----ADVEILEATIVKSVPHKAGYQWFGAFYATTIVTIGYGHSTPMTDAGKVFQM 111

QY 124 AYSVIGIPWNGILFAGLGEYFGRTEA-----IYRKYKYMSTDMHYVPPOLGLITVV 178
DB 112 LVALAGIPLGLIMFOSIGERM-NTPAAKLLRFRRAAGKQPIVTS----- 157

QY 179 IALIPGIALFLVPCGVGHLRELQ-----LSSI-----SLYYSVVTITIGFDYVPT 227
DB 158 -----LIIFCTGWGGLLIFGGAFFSSYENWTYFVAYYCFVLTITIGFDYVAL 207

QY 228 FG-----ANQPKFEGWFFVYQIIVWFIFSLGYL-----VMIMFTITRGLQSK 273
DB 208 QKRSLOQTOPE-----YVFFSLVFLFGLTVISAAMNLLVRLFTMTEDER 254

RESULT 10
T19860
hypoetical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 7.1%; Score 233; DB 2; Length 334;
Best Local Similarity 23.1%; Pred. No. 4.1e-11;
Matches 66; Conservative 62; Mismatches 92; Indels 56; Gaps 10;

QY 5 RWILLIFVISLMEFGAIIYHIEGEEKISRAEORAKQAIANEYLLELGGKNTTQDE 64
DB 10 RALLILSTFTVLLFCAMVFDKLE-----SEKDTWVRDE 43

QY 65 ILQISD-----YCDKVPVLPPTDYDPTWTFYHAFFAFTVCSVGVGNI 111
DB 44 I-ERITDRLKHKYNSERDLHLFAIAIKSIPQAGYQWQFAGAFYATVVTITVGYGHS 102

QY 112 SPTTFAGRMIMAYSIGVIGIPVNGILFAGLGEYFGRTEAIIYRKYKYMSTDMH----- 165
DB 103 APSTWAGKLFQCMIFALGVPMGLIMFQSIGERY-NFTFA-----YSLHFRDLSHQOGFTC 157

QY 166 ----YVPPOLGLITVV--IALIPGIALFLVPCGVGHLRELGLSSISLYSVVTTTIG 220
DB 158 LQEVPTTHLLMVSLTIGFMVIVSGTYME-----HTIEKWSIFD-AIYFCMITFTSIG 208

QY 221 FGDYVPTFGANQPKFEGWFFVYQIIVWF--IFSLGLVLMIMTFTI 265
DB 209 FGDVLPLQOVNALQDQPLVVFATIMFILGLAVFSAACVNLVLLVGM 254

RESULT 11
T24201
hypoetical protein R12G8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24201
R:Basham, V.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19853
A:Accession: T24201
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-485 <WIL>
A:Cross-references: EMBL:Z93782; PIDN:CAB07854.1; GSPDB:GN00023; CESP:R12G8.2
A:Experimental source: clone R12G8
C:Genetics:
A:Gene: CESP:R12G8.2
A:Map position: 5
A:Introns: 74/1; 162/3; 210/1; 288/1; 339/3; 426/3

Query Match 7.1%; Score 232; DB 2; Length 485;
Best Local Similarity 24.8%; Pred. No. 8.1e-11;
Matches 97; Conservative 60; Mismatches 140; Indels 94; Gaps 16;

QY 5 RWILLIFVISLMEFGAIIYHIEGEEKISRAEORAKQAIANEYLLELGD-----KNT 59
DB 92 RYIALLVLAITYLLGATVYFLIEGSNEK-SRLHVRQNL---DKLLDELATVLSAVND 147

QY 60 TTQDEILQISDYCDKVPVLPPTYDD-----TPY-----TWTFYHAFFAFTVCSV 106
DB 148 PQSSEHQMKFFIESYISLQKHEEQYKSTYYRLEHDPDNLKWTFSSAFFSMNVYTTT 207

QY 107 GYGNISPTTFAGRMIMAYSIGVIGIPVNGILFAGLGEYFGRTEAII-----RKYK 159
DB 208 GYGSISAQTFSGQLFTMIYAFCFVPTLVILRDGLQMFVNLTKLYAHGLTAVRRIRGR 267

QY 160 MSTDMHYVPPOLGLITVVIALIPGIALFLVPCGVGHLREL-----GLSSI-SLY 211
DB 268 EYDEDEIIQLPIKFCMTILIA-----YLLCTTFVLYLDVAVMGPEWDDGLPYTAFY 320

QY 212 SVVFTTTTIGFDYVPTFGANQPKFEGWFFVYQIIVWFIFSLGYLVIM-----TFIF 266
DB 321 SFISLTTIGLDVMPNNVYAPP-----VSMIFFIGNAVTKVYNRATFIIV 366

QY 267 -----RGLQSKKILAYLEQQLSSNLKATQN-----RIWSGVY---KDVG 301
DB 367 ENGVFGLMTLAETKISMLLTERKPGVKTVRSTSGSSAERSVDSKEPRGFDGSDSGDDG 426

QY 302 YLRRLNELYILKVPVYTDVDIAVTLPRSN 332
DB 427 VINRRRNEM-----MNTFTVRSIA-TFMRSN 451

RESULT 12
T32347
outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32347
R:Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid F34D6.
A:Reference number: Z21153
A:Accession: T32347
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-336 <WUR>
A:Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
A:Experimental source: strain Bristol N2; clone F34D6
C:Genetics:
A:Gene: twk-23; CESP:F34D6.3
A:Map position: 2
A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
```


121034
121035

A; Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1

Job time: 2044 sec

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Result No.	Query			ID	Description
	Score	Match	Length		
1	215	6.5	335	1 TWK8_CAEEL	P34410 caenorhabdi
2	131.5	4.0	2312	1 CCAE_HUMAN	Q15878 homo sapien
3	127	3.9	691	1 TOK1_YEAST	P40310 saccharomyc
4	122.5	3.7	333	1 Y13B_METJA	Q37604 methanococc
5	115	3.5	637	1 YHE7_YEAST	P38724 saccharomyc
6	114	3.5	2272	1 CCAE_MOUSE	Q61290 mus musculu
7	113.5	3.5	425	1 YOCE_ECOLI	P77031 escherichia
8	111.5	3.4	343	1 YD57_METJA	Q58752 methanococc
9	111	3.4	2222	1 CCAE_RAT	Q07652 rattus norv
10	110.5	3.4	2019	1 C1N5_RAT	P15389 rattus norv
11	110.5	3.4	2490	1 PTND_HUMAN	Q12923 homo sapien
12	105	3.2	552	1 YH8_YEAST	P38799 saccharomyc
13	104	3.2	504	1 RA52_YEAST	P06778 saccharomyc
14	102	3.1	506	1 HITB_HAEIN	P71338 haemophilus
15	102	3.1	1851	1 CCAA_DROME	P91645 drosophila
16	101.5	3.1	390	1 IRKB_MOUSE	Q61743 mus musculu
17	100.5	3.1	390	1 IRKB_HUMAN	Q14654 homo sapien
18	100	3.0	1558	1 YK83_YEAST	P36028 saccharomyc
19	99.5	3.0	334	1 PIT_RHIME	O30499 rhizobium m
20	99.5	3.0	1207	1 DPOL_ASFB7	P42489 african swi
21	98.5	3.0	160	1 KCSA_STRLI	Q54397 streptomyce
22	98.5	3.0	3432	1 POLG_JAEVY	P32886 j genome po
23	98	3.0	522	1 NU5M_MYTED	Q00232 mytilus edu
24	98	3.0	1475	1 TRAZ_CAEEL	P34709 caenorhabdi
25	97.5	3.0	390	1 IRKB_RAT	P70673 rattus norv
26	97.5	3.0	450	1 YOE3_CAEEL	Q17528 caenorhabdi
27	97.5	3.0	676	1 C1O1_HUMAN	P51787 homo sapien
28	97.5	3.0	3432	1 POLG_JAEVY	P27395 j genome po
29	96.5	2.9	570	1 HXT1_YEAST	P32465 saccharomyc
30	96.5	2.9	604	1 C1Q1_MOUSE	P37414 mus musculu
31	96.5	2.9	1227	1 LAF4_HUMAN	P51826 homo sapien
32	95.5	2.9	767	1 HYPF_SYNY3	Q55638 synechocyst
33	95.5	2.9	1794	1 YAV1_SCHPO	Q10172 schizosacch

QY 185 --IALFLVPCGVHLLREGLSSI--SLYSYVYTTTIGRQDGYVPTFGANQPKFGWF 240
Db 136 LVAILIYVTAFCGVLSKLEPWFSTFSYWSFTTMTTGVGDLMP-----RRDGYM 187
QY 241 VYQIFVIVW-----FFSGLYLVMTFTTRGLQ-SKKLAY-----276
Db 188 YIILLYILKFSMKKQKFIKFLGDAITTCIDLVGVQYIRKLTHTFGRTQDARSALAV 247
QY 277 -----LEQQLSSNLKATONRINSVTKDVGYLRRMLNELYLKVKPYTDDVDIATLPR 330
Db 248 VGGKVLVSELYANL--MQRR-----ARMSREAFI--VENLYVSKHIIPIPT 292
QY 331 SNSC 334
Db 293 DIRC 296

RESULT 2
CCAE_HUMAN STANDARD; PRT: 2312 AA.
AC Q15878; Q14580;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM
CHANNEL II) (BII).
GN CACNA1E OR CACNA1A6 OR CACNA1C6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=95236033; PubMed=7536609;
RA Schneider T., Wei X., Olcese R., Costantin J.L., Neely A., Palade P.,
Perez-Reyes E., Qin N., Zhou J., Crawford G.D., Smith R.G.,
Appel S.H., Stefani E., Birnbaumer M.;
RT "Molecular analysis and functional expression of the human type E
neuronal Ca2+ channel alpha 1 subunit.";
RL Recept. Channels 2:255-270(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RX MEDLINE=94350992; PubMed=8071363;
RA Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F.,
Phillipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
RT "Structure and functional characterization of neuronal alpha 1E
calcium channel subtypes.";
RL J. Biol. Chem. 269:22347-22357(1994).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-1IIA (OMEGA-AGA-1IIA).
THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
CONOTOXIN-GVIA (OMEGA-CYX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
IMPORTANT FOR INFORMATION PROCESSING.
CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1E-1 AND ALPHA-1E-3

(SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES AND IN KIDNEY.
-1- DOMAIN: EACH OF THE FOUR INTERNAL REGIONS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
POSSIBLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
-1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; L27745; AAA72125.1; -;
DR EMBL; L29384; AAA59204.1; -;
DR EMBL; L29385; AAA59205.1; -;
DR MIM: 601013; -;
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR002077; -;
DR PRAM: PF00520; Ion_trans; 4;
DR PRINTS: PR00167; CACHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; Alternative splicing.
FT REPEAT 76 354
FT REPEAT 462 706
FT REPEAT 1139 1425
FT REPEAT 1462 1725
FT DOMAIN 1 89
FT TRANSMEM 90 108
FT DOMAIN 109 127
FT TRANSMEM 128 146
FT DOMAIN 147 158
FT TRANSMEM 159 173
FT DOMAIN 174 185
FT TRANSMEM 186 203
FT DOMAIN 206 223
FT TRANSMEM 224 244
FT DOMAIN 245 326
FT TRANSMEM 327 350
FT DOMAIN 351 476
FT TRANSMEM 477 496
FT DOMAIN 497 509
FT TRANSMEM 510 529
FT DOMAIN 530 538
FT TRANSMEM 539 557
FT DOMAIN 558 567
FT TRANSMEM 568 586
FT DOMAIN 587 605
FT TRANSMEM 606 625
FT DOMAIN 626 678
FT TRANSMEM 679 703
FT DOMAIN 704 1147
FT TRANSMEM 1148 1164
FT DOMAIN 1165 1188
FT TRANSMEM 1189 1208
FT DOMAIN 1209 1216
FT TRANSMEM 1217 1239
FT DOMAIN 1240 1253
FT TRANSMEM 1254 1271
FT DOMAIN 1272 1290
FT TRANSMEM 1291 1310
FT DOMAIN 1311 1397
FT TRANSMEM 1398 1421
FT DOMAIN 1422 1478
FT TRANSMEM 1479 1497
FT DOMAIN 1498 1512
FT TRANSMEM 1513 1532

FT DOMAIN 1533 1540
FT TRANSMEM 1541 1559
FT DOMAIN 1560 1570
FT TRANSMEM 1571 1589
FT DOMAIN 1590 1608
FT TRANSMEM 1609 1628
FT DOMAIN 1629 1697
FT TRANSMEM 1698 1723
FT DOMAIN 1724 1732
FT DOMAIN 1716 721
FT DOMAIN 748 753
FT DOMAIN 767 772
FT DOMAIN 1227 1230
FT DOMAIN 2283 2287
FT DOMAIN 374 391
FT SITE 309 309
FT SITE 657 657
FT SITE 1371 1371
FT SITE 1662 1662
FT CA_BIND 426 438
FT MOD_RES 1733 1733
FT CA_BIND 1751 1762
FT CARBOHYD 254 254
FT CARBOHYD 1565 1565
FT CARBOHYD 1570 1570
FT VARSPLIC 748 766
FT CONFLICT 648 648
FT CONFLICT 836 837
FT CONFLICT 1954 1954
FT CONFLICT 1966 2008
FT CONFLICT 2076 2076
FT CONFLICT 2083 2083
FT CONFLICT 2205 2205
FT CONFLICT 2218 2218
FT CONFLICT 2244 2244
SQ SEQUENCE 2312 AA; 261727 MW; 633ED3EFD407D65E CRC64;

Query Match 4.0%; Score 131.5; DB 1; Length 2312;
Best Local Similarity 20.1%; Pred. No. 0.16;
Matches 125; Conservative 92; Mismatches 261; Indels 145; Gaps 26;

Qy 90 WTFYHAF-----FFATVCSVGVGNI-----SPTTFAGRMIMIA 124
Db 1597 WTVQSFALPYVCLLIAMLEFFIYAIIGMQVFGNKLDESHINHNFRSFFGSLMLLF 1656
Qy 125 YSVIGIPVNGILFAGLGYFGRTFE---AIVRYRYKKYKMSDMDHVPQGLLITVVIA 180
Db 1657 RSATGEANQEIIMSLGEG---KGCEPDITATSGQENECGTDLAYV---YFVSFIFFC 1709
Qy 181 LIPGIALFLVL-----PCGVHLLREL-----GLUSSISLYSYVT- 215
Db 1710 SFLMLNLEFVIMDNFEYLTDRSSILGPHLHDFVRVWAEYDRAACGRHIVTEYEMLT 1769
Qy 216 -TTTIGFGDYPTTGANQPKFEGGFVYQIFVI-----VWIFSLGYLVMWTFITRGLQ 270
Db 1770 MSPPLGLGKRCPS-----KVAYKRLVLMNMPVAEDMTVHFTSLMALIRTALD 1817
Qy 271 SK--KLAYLEOOLSSNLKATQNRISGWTGVDGYLRLMLNELYLKVKPVVTDVDI---- 324
Db 1818 IKIAGGADROOLDSELOKETLAIWPHLSQKMLDLVWPMRASDLTVGKIIVAMMIMDY 1877
Qy 325 -----AYTIPRNSCPDLMSYRVEPAPISRRKRAFSSVCADMVGAQREAGMVHANSDT 376
Db 1878 KOSKVKKQROOLEQKNAP--MFQRMFSSLPQEIIANAKALPYLQDDPVSGLSGRSCYP 1935
Qy 377 DLTKLDREKTFE-----TAAAYHQTDTLLAKVVALATVKPP-----PAEQEDAAIYG 424

Db 1936 SMSPLSPQDIFQLACMDTDDCQFQEROSLEPEVSELKSVQSPNHHGIYLPSTQEHAGSG 1995
Qy 425 GYHGFS-----DSQIL-----ASEWSEFTVNETSPRRPRARACSDENLEAP---RMQSERP 473
Db 1996 RASSMPRLTVDPQVVTDPSSMRFSFTIRD---KRSNSSLWEFSEMERSSSENTYKSR- 2050
Qy 474 LRSSHNWTWG---DNOIQIQAFAFNQRYKGOORANGAANSTWVHLEPDALERLNHRV 530
Db 2051 -RSYHSSLRLSAHRLNSDGHKSDTHRSGGRER--GRSKERKHLSPDV--SRCNSEERG 2105
Qy 531 PVASRSSCMVCDVCFPSRRRTPRRIRWASCPWRSRYPRVSSRRKRPDPWTTTTSRRR- 589
Db 2106 TQADWESERRQSRSPSEGRSOTPNRQGTGSLSESIQVSD-----TSTPRRSRQ 2157
Qy 590 -PPVNP-----ICATDAVVRHPS 606
Db 2158 LPPVPPKPRLLSYSSLIRHAGS 2180
RESULT 3
ID TOK1_YEAST STANDARD; PRT: 691 AA.
AC P40310; Q05721;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN OUTWARD RECTIFIER K+ CHANNEL YORK).
GN TOK1 OR DUK1 OR YJL093C OR J0911.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95076716; PubMed=7985424;
RA Miosga T., Witzel A., Zimmermann F.K.;
RT "Sequence and function analysis of a 9.46 kb fragment of Saccharomyces cerevisiae chromosome X.";
RL Yeast 10:965-973(1994).
RN (2)
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=NY13;
RX MEDLINE=95379951; PubMed=7651518;
RA Ketchum K.A., Joiner W.J., Sellers A.J., Kaczmarek L.K.,
RA Goldstein S.A.N.;
RT "A new family of outwardly rectifying potassium channel proteins with two pore domains in tandem.";
RL Nature 376:690-695(1995).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE=96303826; PubMed=8723646;
RA Reid J.D., Lukas W., Shafaatian R., Bertl A., Scheurmann-Kettner C.,
RA Guy H.R., North R.A.;
RT "The S. cerevisiae outwardly-rectifying potassium channel (DUK1) identifies a new family of channels with duplicated pore domains.";
RL Recept. Channels 4:51-62(1996).
RN (4)
RP SEQUENCE FROM N.A.
RX Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M.,
RA Roney G., Barhanin J.;
RT Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OUTWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: SEEM TO BE COMPOSED OF TWO PORES.
CC
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CC EMBL: U11583; AAB65059.1; -
CC PIR: S48921; S48921.
CC SGD: S0001039; TAF1.
CC KW Hypothetical protein; Transmembrane.
CC SQ SEQUENCE 637 AA; 71553 MW; C47AD0F80A35ACEA CRC64;

Query Match 3.5%; Score 115; DB 1; Length 637;
Best Local Similarity 21.3%; Pred. No. 0.5; Indels 74; Gaps 13
Matches 62; Conservative 51; Mismatches 104;

QY 31 EEKISRQQRKAQTAINEXYLEELGDKNTTQDEILQRI----SDYCDKPVTLPTTYDDT 86
Db 7 DNRSSQTKRKNTKCNELAVDEKDDSSPRDEMDKLGKTSLIIRKSELMAKKYD-- 64
QY 87 PYTWTFYHAFPAFTVCSTVGYG-----NISPTTAGRMIMTAYSVIGI---PVN 133
Db 65 --TWOLKAIFLFAFIC-FTAYGLDSSIRGTYMTYAMNSYSAHSLISTVSVIVLMISAVS 121
QY 134 GILFAGLGEVGFTEFAIYRRYKKYKMTDMHVYPPOLGITTV-----IALIPGIAL 187
Db 122 QVIFGGLSDFGR-----LTLFLSVIVLYIVGTIIQSOAVDQRYAAGAV 166
QY 188 FLVLPQCVGVHLLRELGLSSIS----LYYSVYTT-----TTIGFGDVYPTFGANQKPEFG 237
Db 167 FYVYGLVGMQVQLVLMDSNLSKRLFYTLFSPWSPIITTWYSGVVE---AANPLENW 223
QY 238 GWFVYQVQIFVIV-FIPLSGYLVMINTFI-----TRGLQSKKLAY 276
Db 224 SWNIA-----MWAFFPLCCIPILLCMLHMRKVRNDVEWKELODEKSYV 268

RESULT 6
CCAE_MOUSE STANDARD; PRT; 2272 AA.
ID CCAE_MOUSE
AC Q61290;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (BRAIN CALCIUM
DE CHANNEL II) (BII).
GN CACNA1E OR CCHRA1 OR CACNL1A6 OR CAC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE-94350992; PubMed-8071363;
RA Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F.,
RA Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;
RT "Structure and functional characterization of neuronal alpha 1e
RT calcium channel subtypes".
RL J. Biol. Chem. 269:22347-22357(1994).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-

FT	DOMAIN	1243	1256	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1257	1274	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1275	1293	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1294	1313	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1314	1400	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1401	1424	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1425	1481	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1482	1500	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1501	1515	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1516	1535	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1536	1543	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1544	1562	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1563	1573	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1574	1592	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1593	1611	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1612	1631	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1632	1700	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1701	1726	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1727	2272	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1728	2272	POLY-GLU.
FT	DOMAIN	1729	722	POLY-ARG.
FT	TRANSMEM	751	754	POLY-ARG.
FT	DOMAIN	770	773	POLY-GLU.
FT	TRANSMEM	1108	1112	POLY-GLU.
FT	DOMAIN	1115	1118	POLY-GLU.
FT	TRANSMEM	1231	1234	POLY-VAL.
FT	DOMAIN	2244	2247	POLY-ARG.
FT	TRANSMEM	375	392	POLY-ARG.
FT	DOMAIN	310	310	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	TRANSMEM	658	658	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	DOMAIN	1375	1375	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	TRANSMEM	1666	1666	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	DOMAIN	427	439	BY SIMILARITY.
FT	TRANSMEM	1737	1737	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	DOMAIN	1755	1766	BY SIMILARITY.
FT	TRANSMEM	255	255	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	1569	1569	CARBOHYD
FT	TRANSMEM	1692	1692	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DOMAIN	2272	2272	AA; 257233 MW; 70D9200B9E0C87A1 CRC64;
FT	TRANSMEM	310	310	SEQUENCE
FT	DOMAIN	658	658	Query Match
FT	TRANSMEM	1375	1375	Best Local Similarity 19.5%; Pred. No. 3;
FT	DOMAIN	1666	1666	Matches 118; Conservative 86; Mismatches 242; Indels 160; Gaps 25;
FT	TRANSMEM	427	439	90 WTFYHAF-----FFAFTVGVSTVGYGNI-----SPTTFAGRMIMIA 124
FT	DOMAIN	1737	1737	1601 WTFVQSEKALPYVCLLIAMLEFFIYAIIGMQVFGNKLDEESHINRHNFRSFFGSLMLLF 1660
FT	TRANSMEM	1755	1766	125 YSVIGIPVNGILFAGLGEYGRIFE-----AIYRKYKYNKSTDMHYVPPQLGLITTVVIA 180
FT	DOMAIN	255	255	1661 RSATGEAWQIMLSCLGE-----KCEPDTTAPSGONESERCGTDLAYV-----YFVSFFFC 1713
FT	TRANSMEM	1569	1569	181 LIPGIALFLVL-----PCGVHLLREL-----GLSSISLYSYVVT- 215
FT	DOMAIN	1692	1692	1714 SELMLNLFVAVIMDNFEYLRDSSILGPHLDEFVRVWAEYDRAACGRHITYEMEYMLTL 1773
FT	TRANSMEM	2272	2272	216 -TTTIGDGVVPTFGANQPKFGFVYVIFVT-----VWFIFSLGLVLMIMTFTRGLQ 270
FT	DOMAIN	310	310	1774 MSPPLGLGKRCPS-----KVAYKRLVLMNMPVAEDMTVHTSTLMALIRTALD 1821
FT	TRANSMEM	658	658	271 SK--KLAYLEQQLSSNLKATONRTWSVTKDVGYLRLMLNELYLKVKPYTVDVI----- 324
FT	DOMAIN	1375	1375	1822 IKIAGGADROQLDSELSQKETLAIWPHLSQKMLDLLVPMPKASDLTVGKTYAAMIMDIY 1881
FT	TRANSMEM	1666	1666	325 -----AYTLPRNSCPDLSWYRVEPAPIPSKRAFSVCADWVGQAQREAGMVHANSDT 376
FT	DOMAIN	427	439	1882 KQSKVKQROQLBEQKNAP--MFQRMPESSLPOEITANAKALPYLOQDPVSGLSGRSGYP 1939

QY	377	DLTKLDREKTFETAEAYHQTTDLLAKVYNVALATVKVPPPAQEDAAALYGGYHGFSDSOIL- 435
DB	1940	SMSPSQEIFQ-----LACMDPADDGQ-----FQEQQSLV 1970
QY	436	-----ASEWSEFSTVNEFTSPRRPARACSFENLEAP---RWQSERPLRSSHNWTWSG--- 485
DB	1971	VTPSSMRRSFSTIRD---KRSNSSLWLEFSEMSSESTYKSR--RSYHSSLRLSAHR 2024
QY	486	-DNQIOEAFNQRYKGOORANGAANSTMVHLEPDALAEQLRNHRVPAVSRSSPCRMVCD 544
DB	2025	LNSDSGHKSTHRSRGRER--GRSKERKHLSPDV--SRCNSEBGTQADWESPERQSR 2080
QY	545	VCFPSSRSTPRRIWASCPWRSRYPRVSSRRKPDPRWTTTSTRSR--PPVNP-----ICA 597
DB	2081	SPSEGRSOTNRQGTGSLSESSIPSISD-----TSTPRSRRLQPPVPPKPRPLLSY 2132
QY	598	TDAVRH 603
DB	2133	SSLMRH 2138
RESULT	7	
QYCE_ECOLI		STANDARD; PRT; 425 AA.
ID	QYCE_ECOLI	P77031; P76634; P76635;
AC	P77031	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997	(Rel. 35, Last sequence update)
DT	01-NOV-1997	(Rel. 35, Last annotation update)
DE	HYPOTHETICAL 46.8 KDA PROTEIN IN CYSJ-ENO INTERGENIC REGION.	
GN	YQCE.	
OS	Escherichia coli.	
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC	Escherichia.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	STRAIN=K12 / M61655;	
RA	MEDLINE=97426617; Pubmed=9278503;	
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,	
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	
RA	Mau B., Shaoy Y.;	
RT	"The complete genome sequence of Escherichia coli K-12."	
RL	Science 277:1453-1474(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12;	
RA	Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,	
RA	Ikemoto K., Inada T., Isono K., Kimura S., Kitagawa M.,	
RA	Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,	
RA	Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,	
RA	Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,	
RA	Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,	
RA	Yamamoto Y., Yano M.;	
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.	
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).	
-C-	-1- SIMILARITY: TO E.COLI YIHN.	
CC		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC		
DR	EMBL; AE000361; AAC75817.1; --	
DR	EMBL; D90893; CAB22504.1; --	
DR	ECOGENE; EG13174; YQCE.	
KW	Hypothetical protein; Transmembrane.	
FT	TRANSMEM 9 29	POTENTIAL.
FT	TRANSMEM 49 69	POTENTIAL.
FT	TRANSMEM 76 96	POTENTIAL.
FT	TRANSMEM 97 117	POTENTIAL.


```
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 314 334 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
FT TRANSMEM 389 409 POTENTIAL.
SQ SEQUENCE 425 AA; 46830 MW; 538C547C7FC52DEA CRC64;

Query Match 3.5%; Score 113.5; DB 1; Length 425;
Best Local Similarity 20.6%; Pred. No. 0.39;
Matches 59; Conservative 42; Mismatches 105; Indels 81; Gaps 12;

QY 8 LLLIYISYLMFGAIIYHIEGEEKISRAEOKKQAIANEYLLLELGGKNTTODEILO 67
DQ 173 VIIIVSVVILGILCWFFVSNNLRSANNEKQSFQSLDIL-----AVL 218
QY 68 RLSYCDKVPVLPPTDYDPPTFTFHAFFAFTVCSTVGYGNISPTTFAGRMIMIAYSV 127
DQ 219 RIIST-----TWYCSMVIFGVFTIYAILLSYNTLYLTEMYG-MSLVAAASY 260
QY 128 IGIPVNGILFAGLGEYFGRTFEAIYRYKRYKMSYDMHYVPPQLGLITTVW----- 178
DQ 261 MGLVINKIFRALCGPLGG-----LITYSKVKSPTFVIOILSVLGLLTALLVTSNQPQ 315
QY 179 -IALIPGIALFVLPCVGHLLRELGLSSISLY-----SYVTITIGFGDYVPFT 228
DQ 316 SVAMGIGLILLCLFTC-----YASRGLYWACPGEARPTSYIMGTTCVIGSIVGLF 365
QY 229 GANQKPEF-----GGW-----FVYVQIFVIVWF--IFSLGLVLMIMTFPI 265
DQ 366 ----PDVFYPIIGHWQDTLPAAEAYRNMLMGMAALG-MVIVFTPL 407

RESULT 8
YD57_METJA STANDARD; PRT; 343 AA.
AC Q58752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE PUTATIVE POTASSIUM CHANNEL PROTEIN MJ1357.
GN MJ1357.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: STRONG, TO M.JANNSCHII MJ0138.1.
CC -!- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U67575; AAB99365.1; -
DR TIGR; MJ1357; -
KW Hypothetical protein; Transmembrane; Transport; Ion transport;
KW Ionic channel.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 62 82 POTENTIAL.
SQ SEQUENCE 343 AA; 38883 MW; 61231B0C001B54C4 CRC64;

Query Match 3.4%; Score 111.5; DB 1; Length 343;
Best Local Similarity 28.9%; Pred. No. 0.42;
Matches 26; Conservative 21; Mismatches 40; Indels 3; Gaps 2;

QY 92 FYHAFFFAFTVSTGVGYNISPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYF--GRTFE 149
DQ 133 YFTALYFSVITITTCYGDFTPKTFLGRLTLVVYLCVGVIVMFLSLIAEFIVECKFEE 92
QY 150 AIYRYKRYKMYST-DMHYVPPQLGLITTVV 178
DQ 93 FVRLKMKMKIKTKDKHYICGYGRGLGVV 122

RESULT 9
CCAE_RAT STANDARD; PRT; 2222 AA.
AC Q07652;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL ALPHA-1E SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6) (RBE-II) (RBE2)
DE (BRAIN CALCIUM CHANNEL II) (BII).
DE CACNALE OR CACNLIA6 OR CAC46.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=93262464; PubMed=8388125;
RA Soong T.W., Stea A., Hodson C.D., Dubel S.J., Vincent S.R.,
RA Snutch T.P.;
RT "Structure and functional expression of a member of the low voltage-
RT activated calcium channel family."
RL Science 260:1133-1136(1993).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E
CC GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA).
CC THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), OMEGA-
CC CONOTOXIN-GVIA (OMEGA-CTX-GVIA), AND OMEGA-AGATOXIN-IVA (OMEGA-
CC AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE
CC INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS
CC IMPORTANT FOR INFORMATION PROCESSING.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM AND IN
CC INSULINOMA.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
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POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION. -I- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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 EMBL: L15453; AAA0855.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR002077; -
 DR PFAM: PF00520; Ion_Trans; 4.
 DR PRINTS: PRO0167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation.
 FT REPEAT 27 305 I.
 FT REPEAT 413 657 II.
 FT REPEAT 1092 1378 III.
 FT REPEAT 1415 1678 IV.
 FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 41 59 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 60 78 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 79 97 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 98 109 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 110 124 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 125 136 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 137 156 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 157 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 195 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 196 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 302 427 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 428 447 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 448 460 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 461 480 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 481 489 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 490 508 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 509 518 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 519 537 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 538 556 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 557 576 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 577 629 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 630 654 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 655 1100 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1101 1117 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1118 1141 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1142 1161 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1162 1169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1170 1192 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1193 1206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1207 1224 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1225 1243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1244 1263 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1264 1350 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1351 1374 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1375 1431 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1432 1450 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1451 1467 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1468 1485 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1486 1493 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1494 1512 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1513 1523 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1524 1542 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1543 1561 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1562 1581 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1582 1650 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	1651	1676	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1677	2222	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	667	672	POLY-GLU.
FT	DOMAIN	699	704	POLY-ARG.
FT	DOMAIN	718	723	POLY-ARG.
FT	DOMAIN	1058	1064	POLY-GLU.
FT	DOMAIN	1180	1183	POLY-VAL.
FT	DOMAIN	2193	2196	POLY-ARG.
FT	DOMAIN	325	342	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	SITE	260	260	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	608	608	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1324	1324	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1615	1615	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CA_BIND	377	389	BY SIMILARITY.
FT	MOD_RES	1686	1686	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1704	1715	BY SIMILARITY.
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1523	1523	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1641	1641	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	2222	2222	AA; 252114 MW; DP6452A2175CEB19 CRC64;

Query Match 3.4%; Score 111; DB 1; Length 2222;
 Best Local Similarity 19.3%; Pred. No. 4.9;
 Matches 117; Conservative 87; Mismatches 242; Indels 160; Gaps 25;

QY	90	WTFVHAF	-----FFAFTVCSTVGNY	-----SPTTEAGRMIMIA	124
QY	1550	WTFVQSKALPYVCLLIAMFFIYAIIGMOVFNKIDDESHNRNNRNFSPFGSLMLLF	1609		
QY	125	YSVIGIPVNGILFAGLGEYEGRTFE	-----AIYRKYKYMSTDMHYVPPOLGLITTVIA	180	
QY	1610	RSATGEAWQEIIMLSCLGE	-----KCEPDTTAPSGONESERCGTDLAVY	-----YFVSFIFFC	1662
QY	181	LIPGIALFLVL	-----PCVGVHLLREL	-----GLSISLYSVVT	215
QY	1663	SFLMLNLFVAVIMDNFEYLTROSSILGPHLDEFVRVWAEYDRAACGRHITYEMEYELT	1722		
QY	216	TTTIGFGDYVPTFGANQPKFEGGVVYQIFVI	-----VWFIESLGLVLMIMFTIRGLQ	270	
QY	1723	MSPLGLGKRCPS	-----KVAYKRLVLMNMPVAEDMTVHTSTLMALIRTALD	1770	
QY	271	SK-KLAYLEQQLSSNLKATQNRISGVTKDVGYLRRMLNELYLKVKPYTVDVI	-----324		
QY	1771	IKIAGGADRQQLDSELOKETLAIWPHLSQKMLDLLVPMKASDLTVGKIYAAMIMDYY	1830		
QY	325	-----AYTLPRNSCPDLSMYRVEPAPISPKRAFSVCADMVGAQRAAGVHANSDT	376		
QY	1831	KQSKVKKQROQLBEQKNAP	-----MFQRMPPSLPQEIISNAKALPYLQDDPVSGLSGRSGYP	1888	
QY	377	DLTKLDREKTEFAEAYHQTDLAKVNAVALTKVPPAEQDAALYGGVHGFSQIL	435		
QY	1889	SMSPLSPQEIFQ	-----LACMDPADGQ	-----FQEQQLV	1919
QY	436	-----ASEWSFTVNFTSPRRPRACSDFNLEAP	-----RWQSERPLRSHNWTWSG	-----485	
QY	1920	VTDPSMRSRSTIRD	-----KRSNSSLWLEFSEMSERSENTYKSR	-----RSVHSLRLSAHR	1973
QY	486	DNQIQEAFNQRYKGOQRANGAANSTWVHLEPDALBEOQLNNHNPVVASRSPCRMVCD	544		
QY	1974	LNSDSGHKSDTHRSGRER	-----GRSKERKHLSPDV	-----SRCNSEERTQADWESPERRQR	2029
QY	545	VCPPSRSTPRRTWSASCWPSRYPRVSSRRKPDPRWTTTSTRSR	-----PPVNP	-----ICA	597
QY	2030	SPSEGRSQTPNRQGTGSLSESSIPSISD	-----TSTPRRSRRLQPPVPPRPLLSY	2081	
QY	598	TDAVRH	603		

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
Vignati D., Wilcox L., Wohlman P., Waterston R., Willson R.,
Vaudin M.;
RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
VIII.";
RL Science 265:2077-2082(1994).
RC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC
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CC
CC
DR EMBL; U10556; AAB68887.1; -
DR PIR; S46809; S46809.
DR SGD; S0001120; YHR078W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 127 147 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT TRANSMEM 393 413 POTENTIAL.
FT TRANSMEM 517 537 POTENTIAL.
SQ SEQUENCE 552 AA; 63330 MW; 8FE0AE88937E281F CRC64;

Query Match 3.2%; Score 105; DB 1; Length 552;
Best Local Similarity 21.6%; Pred. No. 2.3; Mismatches 50; Indels 90; Gaps 14;
Matches 68; Conservative 50;
QY 31 EKISRAEQRKAQ-TAINFYLLLEELGDKNTTQDEILQRIISYCDKVPPLPPTDDTPYT 89
DB 256 EEKIQDYEHNEIQNQLRSLEEVEE-NSTFKAELEMKIANVQLEGLKLEALLQSPQV 314
QY 90 WTFYHAF---FFAFTVCSVGVGNISPTTFAGRMIMAIYSGIPVN-----133
DB 315 RTFKAFGEFTIYCLHKLI-----ITFLKRIPIYIYHSLKYPDDYDNFSENAASD 367
QY 134 --GILFAGGEVGRFTEAIYRRYKMKSTDMHYVPPOLGLI-----TTV 177
DB 368 PLATIANILDF-----SFFRFNYQHDLSLTKQISLSLSLFLCCLSAVNTTI 417
QY 178 --VIALIP---GIALFL-----VLP-----CVGVHLLRELGLS 205
DB 418 SYVVTLLPKFKQILALFAMQNDTANVLPETYNNSYKGGKKNYSOEQKGISLKNLVVS 477
QY 206 SISLYSYVTTTIGDGVPTFEGANQPKF-EGGVFVYQIIVVWF-----IFSLGYLVW 260
DB 478 ELT--GVVYLATLVMRSHLPFVSORLKGKLGKFTVPNIIVDSWDFEVYAFACVFTFI 535
QY 261 IMFTITRGLQSKLA 275
DB 536 CIRIAERKLSTKKVS 550

RESULT 13
RA52_YEAST
ID RA52_YEAST STANDARD; PRT; 504 AA.
AC P06778;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE DNA REPAIR AND RECOMBINATION PROTEIN RAD52.
GN RAD52 OR YHL032C.

OS *Saccharomyces cerevisiae* (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; *Saccharomycetes*; *Saccharomycetales*;
OC *Saccharomycetaceae*; *Saccharomyces*.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85137465; PubMed=6098821;
RA Adzuma K., Ogawa T., Ogawa H.;
RT "Primary structure of the RAD52 gene in *Saccharomyces cerevisiae*.";
RL Mol. Cell. Biol. 4:2735-2744(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN DOUBLE-STRAND BREAK (DSB) REPAIR AND
CC RECOMBINATION.
CC -!- SUBUNIT: PART OF A COMPLEX THAT INCLUDES RAD51 AND RAD52.
CC -!- SIMILARITY: BELONGS TO THE RAD52/RAD22 FAMILY.
CC
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CC
CC
DR EMBL; M10249; AAA50352.1; -
DR EMBL; Z46659; CAA86623.1; -
DR PIR; A23282; A23282.
DR SGD; S0004494; RAD52.
KW DNA recombination; DNA repair.
SQ SEQUENCE 504 AA; 56063 MW; 590C3700B1B8058 CRC64;

Query Match 3.2%; Score 104; DB 1; Length 504;
Best Local Similarity 18.7%; Pred. No. 2.4; Mismatches 71; Indels 166; Gaps 24;
Matches 96; Conservative 71;
QY 192 PCGVGH-----LRELGLSISLSYSYVTTTITGFGD-----YVPTFG---ANPKPF 236
DB 45 PVFGNHSEDIQTKDKKLGPEYIS-----KRVGFGTSRTAYIEGWRVINLANQIFY 96
QY 237 GGFVYVYQIVVWFI-----FSLGYLVIMTFTIRGLQSKLAYLEOOLSSNLKATON 290
DB 97 NGWSTEVK-SVVIDFLDERQGFSGICTAIVRVTLTSGTYREDIGYGTVENERRKPAAFE 155
QY 291 RIWSGVTKDV-----GYLRRLNELY-----ILKVK-----PVYTDVDIAYTL 328
DB 156 RAKKSAVTDAKRSURGFNGALGNCLYDKFLAKIDKVKFDPDPDENLFRPTDISES 215
QY 329 PRNSPCDLSMYRVEPAPIPSRKRAFSCVAD-----MVGAREA 367
DB 216 SRTNLTHE---NQEQOQYPNKRRLTKVTNTNPDSKTNLVKIENTIVSRGTPMMAAPAE 271
QY 368 GMVH-ANSDTDTLKDREKTFTAEAYHQTDLAKVVALATVPKPPAEQEDAAALGYG 426
DB 272 NSKNSNKNKDTLKLSDASK-----QQQDOLL-----DDSLMFS-- 304
QY 427 HGFSDSOILASEWSFSTVNEFTSPRP-----RARACSDFNLEAPRWQSERPLRSSHNEW 481
DB 305 DDFQDDLLI--NMGNTNSNVLTEKDPVVAKOSPTASSNPEAEITFTVAKAATSQVNE- 361
QY 482 TWSGDNQIQEAFNORYKGQORANGAANSTMVHLEPDALDEO-----523
DB 362 RYIGE-----ESIFDPKYQAOISRHTVDQTTSKHIPASVLKDKTWTARDVSVEKFAPKG 417
QY 524 ----LRNN-----HRVPVASRSSPCRMVCDVCFPPSRRTPRRIWSASCPSWRYPRVSSR 574
DB 418 QLSMKNNDKELGPHMLEGAGNQVP-----RETTPIKTINATAFPPAAAPRAPPS 466
QY 575 K---PD-----PRWTTTSTRSRPPVNPICA 597

Db 467 KWHPNGNGAVPAVPOQRSTREVRKPNPLHA 500

RESULT 14

HITB_HAEIN STANDARD; PRT; 506 AA.
AC P71338; Q53440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN HITB.
GN HITB OR HI0098.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-L., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NTHI TN106;
RX MEDLINE=95012644; PubMed=7927717;
RA Sanders J.D., Cope L.D., Hansen E.J.;
RT "Identification of a locus involved in the utilization of iron by
RT Haemophilus influenzae.";
RL Infect. Immun. 62:4515-4525(1994).
CC -1- FUNCTION: INVOLVED IN A PERIPLASMIC BINDING-PROTEIN-DEPENDENT
CC IRON(III) TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (POTENTIAL).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U32695; AAC21774.1; ALT_INIT.
DR EMBL; S72674; AAB32111.1;
DR TIGR; HI0098;
DR INTERPRO; IPR000515;
DR PRAM; PF00528; BPD_transp. 2.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
DR TRANSPORT; Iron transport; Transmembrane; Inner membrane.
FT TRANSEM 9 29 POTENTIAL.
FT TRANSEM 57 77 POTENTIAL.
FT TRANSEM 90 110 POTENTIAL.
FT TRANSEM 116 136 POTENTIAL.
FT TRANSEM 174 194 POTENTIAL.
FT TRANSEM 218 238 POTENTIAL.
FT TRANSEM 275 295 POTENTIAL.
FT TRANSEM 314 334 POTENTIAL.
FT TRANSEM 350 370 POTENTIAL.
FT TRANSEM 379 399 POTENTIAL.
FT TRANSEM 428 448 POTENTIAL.

FT TRANSEM 480 500 POTENTIAL.
FT VARIANT 72 F -> L (IN STRAIN TN106).
FT VARIANT 104 G -> C (IN STRAIN TN106).
FT VARIANT 116 V -> G (IN STRAIN TN106).
FT VARIANT 167 S -> F (IN STRAIN TN106).
FT VARIANT 252 T -> M (IN STRAIN TN106).
SQ SEQUENCE 506 AA; 56546 MW; ADA28861C1481A1D CRC64;

Query Match 3.1%; Score 102; DB 1; Length 506;
Best Local Similarity 22.3%; Pred. No. 3.4;
Matches 66; Conservative 46; Mismatches 112; Indels 72; Gaps 13;

QY 3 PNRRILLIFVISYLMFGAALYYHIEGEEKISRAEO-----RKAQIAINEYLLE----- 52
DB 5 PPFWLTLLIILIGLPCLPFLYVILRATEVGLTRSVELLFRPRMAELSLTMLMVCVTI 64
QY 53 ---ELGDKNTTODEILQRI-----SDYCDKPVTLP---PTYDDTPYTWTYHAFFFAFTV 102
DB 65 GAISLG---TFCAFLLERYRFFGKAFFEVAMTLPICIPAF-VSGFTW-----ISLTF 112
QY 103 CSIVGYGNISPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYFGRTFAIYRRYKYYKMS 162
DB 113 RVEVFWGTI-----GIMTSSFPFLAYLPVSAIL-----KRLDRSLEEVSLSGKSPV 161
QY 163 DMHVVPOLGLITTVTIALIPGIALFLVPCVGVHLLRELGLSSLSYYSVYVTTTIGFG 222
DB 162 FWAISPOLK-----PATGSSILL--IALHMLVEFGAVSI---LNYQFTTAIFQ 206
QY 223 DYVPTFGANQPKFEGWVYVYFIVWFIFSLG-----YLVMMINTF 264
DB 207 EYEMSFNNSTAALLSAVLMAICILIVFEGEIFFRKGQTLVHSGKGVTRPYLVKLTSLF 262

RESULT 15
ID CCAA_DROME STANDARD; PRT; 1851 AA.
AC P91645; O01713; O01714;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-DEPENDENT CALCIUM CHANNEL TYPE A ALPHA-1 SUBUNIT (CACOPHONY
DE PROTEIN) (NIGHTBLIND A PROTEIN) (NO-ON-TRANSIENT B PROTEIN) (DMCALA).
GN NBA OR CAC OR NONB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A., AND RNA-EDITING.
RX MEDLINE=97141514; PubMed=8987815;
RA Smith L.A., Wang X.J., Peixoto A.A., Neumann E.K., Hall L.M.,
RA Hall J.C.;
RT "A Drosophila calcium channel alpha subunit gene maps to a genetic
RT locus associated with behavioral and visual defects.";
RL J. Neurosci. 16:7868-7879(1996).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=97247730; PubMed=9093853;
RA Peixoto A.A., Smith L.A., Hall J.C.;
RT "Genomic organization and evolution of alternative exons in a
RT Drosophila calcium channel gene.";
RL Genetics 145:1003-1013(1997).
RN [3]
RP VARIANT CAC-S.
RX MEDLINE=98315104; PubMed=9649530;
RA Smith L.A., Peixoto A.A., Kramer E.M., Vilella A., Hall J.C.;
RT "Courtship and visual defects of cacophony mutants reveal functional
RT complexity of a calcium-channel alpha subunit in Drosophila.";
RL Genetics 149:1407-1426(1998).
CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE


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QY 150 AIYRYKXKXMDHYVPPQLGLTTWVIALIPGIALFLVPCVGVHLLRELGLSSISL 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1256 NSITRHNHQ-----SFIHGV-MLLFRCATGEAWPNIMLACK- 1292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 210 YYSVTTTTTIGFYVTFGANQKKEGGEVYQIVVWFIFSLGYLV-----IM- 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1293 -----GKACDDDAEKAFGEYCGSTLAYAYEVS--FIFCFLMLNLFVAVIMD 1338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 --FTITRGLQSKLAYLEQOLSSNLKATQNRWS-----GVTKDVGYLRRMLNELY-ILKV 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1339 NFDYLTROSSILGANHHDEFV-----RINAEYDPGATGKIHY-----TEMIDMLK- 1383
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 KPVYTDVIAITLPRNSRSCPDLSMYRV---EPAPIPSRKRAFSVCADMVGAQREAGMVHA 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1384 -----NMDPPLGFGNKCPRNLAYKKLIRNMPLDDELRY-QETTTLFALIRENLSIKM 1435
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 373 NSDIDLKLDREKTFEPAEAYHOTDILLA-KVYNALATVKPPPAEQED-----AALYGG 425
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1436 RAPEEMDQAD----MELRETITNIWPLQAKMLNLLV---PPSDQLNKGKLSVGKIYAG 1487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 426 YHGFSDSQILASEWSFSTVNEFTSPRPRACSDFNLEAPRWQSERPLRSSHNEWTWSG 485
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1488 F-----LILESRRSTRFGQL-----DSGMPM----- 1508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 486 DNOQIOEAFNQRYKGQORANGAANSTWVHLEPDALERLNNHR-----VPVASRS 536
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1509 --LELQDA--SRHPSQBSLTGADAG---HLHPG---HSYMNHRRSPSLRHNGSPLARSP 1558
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 537 SPCR-----WVCDVCFP-----SRRSTPRRIWSASCPSRSPRS 571
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1559 SPRRRGHQYIHHDIGFSDTVSDVVMYKETRHPRHGNSHPRYPCGGSWSASTSPARSPPS 1618
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 572 -----SRRK-----PDPRWTTS--TRESRP 590
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1619 RYGHLSRSRRTQLPYPTGTTLQCQRSP 1649

```

Search completed: March 17, 2001, 20:05:16
Job time: 473 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 19:56:18 ; Search time 71.86 Seconds
(without alignments)
1007.995 Million cell updates/sec

Title: US-08-816-011c-2
Perfect score: 3283
Sequence: 1 MSPNRWILLIIFYSYLMFG.....DAVHRHPSNRMAAWPAAAG 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL15:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2652	80.8	1001	5	Q94526
2	308.5	9.4	502	11	Q9JK62
3	301.5	9.2	398	11	O88454
4	301	9.2	499	4	O95279
5	299.5	9.1	411	11	P97438
6	295.5	9.0	426	4	O95069
7	295.5	9.0	538	11	Q9J1S4
8	292.5	8.9	411	4	Q9NRT2
9	286	8.7	419	4	Q9NYG8
10	264.5	8.1	551	5	O20673
11	264.5	8.1	555	5	O76789
12	264	8.0	393	5	Q9XU07
13	251.5	7.7	336	11	O922T2
14	247	7.5	523	5	O17935
15	245.5	7.5	336	11	O08581
16	242	7.4	374	4	O9NPC2
17	242	7.4	452	5	O93531
18	241.5	7.4	340	5	Q9VHE0
19	239	7.3	299	11	Q9QX34

20	239	7.3	336	4	O00180	O00180 homo sapien
21	239	7.3	409	11	O35111	O35111 mus musculus
22	239	7.3	411	11	O54912	O54912 rattus norv
23	238.5	7.3	364	5	O76790	O76790 caenorhabdi
24	237	7.2	365	11	O9JL58	O9JL58 cavia porce
25	237	7.2	395	11	O9JLD4	O9JLD4 rattus norv
26	235	7.2	398	5	Q9VFS9	Q9VFS9 drosophila
27	233.5	7.1	329	5	O76795	O76795 caenorhabdi
28	232	7.1	485	5	O9XTV6	O9XTV6 caenorhabdi
29	231.5	7.1	394	4	O14649	O14649 homo sapien
30	231	7.0	336	5	O17185	O17185 caenorhabdi
31	229.5	7.0	631	5	O45894	O45894 caenorhabdi
32	229	7.0	461	5	Q9TZP8	Q9TZP8 caenorhabdi
33	229	7.0	654	5	P90863	P90863 caenorhabdi
34	227.5	6.9	259	6	O02821	O02821 oryctolagus
35	226	6.9	307	5	O94253	O94253 caenorhabdi
36	223.5	6.8	325	5	O18120	O18120 caenorhabdi
37	223	6.8	513	5	Q22940	Q22940 caenorhabdi
38	222.5	6.8	586	5	O62209	O62209 caenorhabdi
39	220.5	6.7	504	5	Q93732	Q93732 caenorhabdi
40	220.5	6.7	539	5	Q21505	Q21505 caenorhabdi
41	217.5	6.6	643	5	O9XXF6	O9XXF6 caenorhabdi
42	216	6.6	1136	5	O9XX01	O9XX01 caenorhabdi
43	212	6.5	995	5	Q9W2L7	Q9W2L7 drosophila
44	211.5	6.4	484	5	Q9TZP7	Q9TZP7 caenorhabdi
45	211.5	6.4	519	5	Q21467	Q21467 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q94526	PRELIMINARY;	PRT;	1001 AA.
AC	Q94526;			
DT	01-FEB-1997 (Tremblrel. 02, Created)			
DT	01-JAN-1999 (Tremblrel. 09, Last sequence update)			
DE	01-OCT-2000 (Tremblrel. 15, Last annotation update)			
DE	OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (ORK1 PROTEIN) (TWO P			
DE	DOMAIN POTASSIUM CHANNEL ORK1).			
CN	ORK1.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	NCHL TaxID=7227;			
OC	NCBI TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Beres P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LARVA:
RX MEDLINE=97075152; PubMed=8917578;
RA Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.;
RT "Ork1, a potassium-selective leak channel with two pore domains cloned
RT from *Drosophila melanogaster* by expression in *Saccharomyces*
RT cerevisiae";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
CC -1- FUNCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT
CC ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY
CC RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS
CC IS REVERSED.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST
CC EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
CC IN LARVA AND EMBRYO.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC EMBL: AE003484; AAF47972.1; -
CC EMBL: U55321; RAC8250.1; -
CC FLYBASE: FBgn0017561; Ork1.
CC INTERPRO: IPR000099; -
CC INTERPRO: IPR001622; -
CC PFAM: PF02034; TWIK channel; 1.
CC PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein;
KW Potassium transport.
FT DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 7 27 POTENTIAL.
FT DOMAIN 95 111 PORE-FORMING (POTENTIAL).
FT TRANSMEM 120 140 POTENTIAL.
FT DOMAIN 141 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 208 224 PORE-FORMING (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 1001 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1001 AA; 109289 MW; 09AE1A366907E07 CRC64;

Query Match 80.8%; Score 2652; DB 5; Length 1001;
Best Local Similarity 90.9%; Pred. No. 8.6e-202;
Matches 518; Conservative 10; Mismatches 32; Indels 10; Gaps 4;

QY 1 MSPNRWLLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTT 60
DB 1 MSPNRWLLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTT 60
QY 61 TQDEILQRISDYCDKPVLTPTTDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRM 120
DB 61 TQDEILQRISDYCDKPVLTPTTDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRM 120
QY 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKMKSTDMHYVPPOLGLITVWIA 180
DB 121 IMIAYSIGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKMKSTDMHYVPPOLGLITVWIA 180

QY 181 LIPGIALFLVPCVGVHLLRELGLSSLSISLYSYVTTTIGFGDYVPTFGANQPKFEGGW 240
DB 181 LIPGIALFLVPCVGVHLLRELGLSSLSISLYSYVTTTIGFGDYVPTFGANQPKFEGGW 239
QY 241 VYQIFVWVFIFSLGVLVMTFITRGLQSKKLAYLEQQLSSNLKATONRINSGVTKDV 300
DB 240 VYQIFVWVFIFSLGVLVMTFITRGLQSKKLAYLEQQLSSNLKATONRINSGVTKDV 299
QY 301 GYLRRMLNELYLKVKPVYTDVDTIATLPRSNPCDLSMYRVEPAPISPKRAPSVCADM 360
DB 300 GYLRRMLNELYLKVKPVYTDVDTIATLPRSNPCDLSMYRVEPAPISPKRAPSVCADM 359
QY 361 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYHQTDLAKVYNALATKVPKPAEQEDA 420
DB 360 VQAQREAGMVHANSDDTLTKLDREKTFETAEAYHQTDLAKVYNALATKVPKPAEQEDA 419
QY 421 ALYGGYHGFSDSOILASEWFSFSTVNEFTSPRRPRARACSDFNLEAPWQSERPLRSSHNE 480
DB 420 ALYGGYHGFSDSOILASEWFSFSTVNEFTSPRRPRARACSDFNLEAPWQSERPLRSSHNE 479
QY 481 WTWSGDNQOIQEAFNORYKGOQRANGAANSTMVHLEPDALDEEOLRNHRVPAVSRSPPCR 540
DB 480 WTWSGDNQOIQEAFNORYKGOQRANGAANSTMVHLEPDALDEEOLK--QSPGAGRKKFS 537
QY 541 MCVDDV--CFPSRRSTP-----RRIWSASCP 563
DB 538 MPDGLRLRFPFOKKRPSQDLERKLSVVVSP 567
RESULT 2
QY 09JK62 PRELIMINARY; PRT; 502 AA.
AC 09JK62;
DT 01-OCT-2000 (TtEMBLrel. 15, Created)
DT 01-OCT-2000 (TtEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TtEMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL TASK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SVJ; TISSUE=KIDNEY;
RT Roux J., Barhanin J.;
RL "Mouse two p domain potassium channel TASK2";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF259395; AAF68668.1; -
SQ SEQUENCE 502 AA; 55976 MW; E4C7E7CC71B44D95 CRC64;

Query Match 9.4%; Score 308.5; DB 11; Length 502;
Best Local Similarity 23.8%; Pred. No. 2.8e-16;
Matches 134; Conservative 86; Mismatches 214; Indels 129; Gaps 21;

QY 4 NRWILLIFVSYLMFGAAIYHIEHGEKISRAEQKQAIATNEYLLEELGDKNTTQD 63
DB 3 DRGPLLTSAIFVLAIGAAIFVLEERPHWK----EAKNYYTQKLLHKEFPCLSQEGLD 58
QY 64 EILQRISDYCDKPVLTPTTDDTPYTWTFYHAFFAFTVCTVGYGNISPTTAGRMIMI 123
DB 59 KILQVYSDAADQGVAI--TGNQTFNNWNPNAIFAATVITTTIGYGNVAPKTPAGRLFCV 116
QY 124 AVSIVGIPVNGILFAGLGEYFGRTFEAIYRRYKRYKMKSTDMHYVPPOLGLITVWIALIP 183
DB 117 FYGLFGVPLCLTWISALGKFFG-----GRAKRLQGLTRRCVSLRKAQITCAITFVW 169
QY 184 GIALFLVPCVGVHLLRELGLSSLSISLYSYVTTTIGFGDYVPTFGANQPKFEGGWV 243
DB 170 GVLVHLVIPPV-FVMVTEENWNYIEGLYSFILTISTIGFGDFA--GVNPS---ANYHALY 223
QY 244 QIFVIVWVFIFSLGVLVMTFITRGLQSKKLAYLEQQLSS--NLKATONRINS 294

Db 224 RYFVELWYGLAWLSLFVNMKVSMEVHKAIKRRRRKESFESSPHSRKALQ-MAGS 282
QY 295 GYTKDVGYLRLMLNELYLKVKPVYTDV-----DIA 325
Db 283 TASKDVNIFS-----FLSKBEETNDLQKIGKKAMKTSGGGERVPGPHGLGPOGDRL 336
QY 326 YTLPSNSCPDLMSYRVEPAPISPKRAFSVCADMVGAQREAGMVHANSDDLTLKLDREK 385
Db 337 PTIPAS-----LAPLVVYSKNR-----VPSLEEVSOTLKNKGHVSRPLGEEA 378
QY 386 TFEAEAYHQTTDLAKVUNLATV--KPPPAEQEDAALYGGYH----- 427
Db 379 GAQAPKDSYQTFSEV--INQLDRISEGEPWEALD-----YHPLIFQANITENEET 429
QY 428 GFSQSILASEWSFTVNEFTSPRRPRACSDFNLEAPRWSERPLRS-----SHNEWT 482
Db 430 GLSDETSKTS-----SVEDNLTSKEQPE-----QGP--MAEAPLSSTGTFPPSDEST 474
QY 483 WSGDNQIQIEAFNQRYKGOQRAN 505
Db 475 FTSELSVVPYEQLMNEYKNAD 497
RESULT 3
ID O88454 PRELIMINARY; PRT; 398 AA.
AC O88454;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TWIK-RELATED ARACHIDONIC ACID-STIMULATED POTASSIUM CHANNEL PROTEIN TRAAK.
GN KCNK4 OR TRAAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98292450; PubMed=9628867;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.,
RA "A neuronal two p domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids."
RT EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION.
RX MEDLINE=98254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels."
RN Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: VOLTAGE INSENSITIVE. INSTANTANEOUS. OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH EXTERNAL K+ CONCENTRATIONS.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM TRAAK (SHOWN HERE) AND ISOFORM TRAAK2 ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND TESTIS.
CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
DR EMBL; AF056492; AAC40181.1; -.
DR MGD; MG1:1298234; Kcnk4.
DR INTERPRO; IPR000099; -.
DR IPR001622; -.
DR PFAM; PF02034; TWIK_channel; 1.

PRINTS: PR01333; 2POREKCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing; Phosphorylation. CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 3
FT TRANSMEM 4 24
FT DOMAIN 89 113
FT TRANSMEM 119 139
FT DOMAIN 140 171
FT TRANSMEM 172 192
FT DOMAIN 198 222
FT TRANSMEM 235 255
FT DOMAIN 256 288
FT MOD_RES 146 146
FT MOD_RES 262 262
FT MOD_RES 265 265
FT MOD_RES 284 284
FT MOD_RES 288 288
FT MOD_RES 340 340
FT MOD_RES 358 358
FT MOD_RES 360 360
FT MOD_RES 379 379
FT MOD_RES 383 383
FT MOD_RES 383 383
FT CARBOHYD 81 81
FT CARBOHYD 84 84
FT VARSPLIC 63 67
FT VARSPLIC 68 68
SQ SEQUENCE 398 AA; 43051 MW; 478A834B78AEC92 CRC64;
Query Match 9.2%; Score 301.5; DB 11; Length 398;
Best Local Similarity 27.7%; Pred. No. 7.4e-16;
Matches 91; Conservative 51; Mismatches 111; Indels 75; Gaps 10;
QY 7 ILLIFYSYLMFGAIIYHIE-----HGEKISRAEQKQAIANEY---LL 51
Db 7 LALLALVLLVSGALVFQALEQEPHEQQAQKMDHGRDQFLRDHPCVSKSEDFIKLV 66
QY 52 EELGDKNTTQDEILQISDCPKVTPPTDYDDPYTWTFYHAFFAFTVSTGYGNI 111
Db 67 EALGG-----ANPETSNTSSNHNSSAWNLSGAFFSFTITTYGNGI 110
QY 112 SPTTFAGRMITAYSVIGIPVNGILFAGLGEYFGRT-----FEAIIYRYKKYKMTDM 164
Db 111 VLHTDAGRFLFCIFYALVGIPFGMLLAGVGDRLGSLRGIGHIEAIFLKW----- 161
QY 165 HYVPQGLITTVVIALIPGIALFLVLPVGVHLLRELGLSSISLYSYVTITTTGFGDY 224
Db 162 -HVPGLVRSLSAVLFLGLLGLLFLVTPTF-VFSYMSWSKLEAIYFVITVTTTGFY 219
QY 225 VPTFGANQPKFQGVVYQIEVIVWFIFSLGYLVIMFTFTRGLQS-----KKLAYLE 278
Db 220 VPDGDTGQNSP-----AYQPLVFWFLGLAYFASVLTITGNWLRVSRRAEMGGLT 273
QY 279 QQLSSNLKATQNRWSG-----VTKDVG 301
Db 274 AQAAS-----WTGTVTARVQTGT 292
RESULT 4
ID O95279 PRELIMINARY; PRT; 499 AA.
AC O95279;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK-2.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;


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FT DOMAIN 129 155 PORE-FORMING (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 311 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 300 300 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 303 303 PHOSPHORYLATION (BY CAM-KINASE II)
(POTENTIAL).
FT MOD_RES 328 328 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 333 333 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 345 345 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DDDD103EFA05 CRC64;

Query Match
Best Local Similarity 9.1%; Score 299.5; DB 11; Length 411;
Matches 110; Conservative 72; Mismatches 151; Indels 95; Gaps 18;

Qy 9 LLFIYISYLMFGAALYYHIEGEEKISRAEQKQAIAINEYLLELGDKNNTTQDEILQR 68
Db 50 IFLVVVLYLIIGAAVFKALEQPQE---ISQRTTIVIOKQTFIAQHACVNSTELDELIOQ 105
Qy 69 ISDYCDKPVTLPTDDTPYTWTFYHFAFFAFTVCGTGVGNISPTTFAGRMIMTAYSVI 128
Db 106 IVAAINAGIILPLGNSNQVSHWDLGSSFFACTVTTTIGFNGNISPTTEGKIFCIYALL 165
Qy 129 GIPVNGILFAG---LGEVFGRTFAIYRYKKYKMSDTHVVPQGLGLITTVIALIPG 184
Db 166 GIPLEFGLLAGVDQGLTIFGKIAKVEDTFIKNVS-----QTKIRIISTIIILF-G 218
Qy 185 IALFLVLPVCGVHLLREL-GLSSI-SLYSYVYVTTTTIGFDYVPTFGANQPKFGWV 242
Db 219 CVLFVALPAV---IFKHIEGNSALDAIVFVITLTIGFDYVA-----GSDIE 265
Qy 243 YQIFV-IWVF--IFSLGYLWMTFIRGLQ--SKLAYLEQQLSSNLKATQNRWISGV 296
Db 266 YLDFYKPVVWFILVGLAYFAVLSMIGDLRVISKK-----TKEEVGFRAHAETWAV 321
Qy 297 TKDVGYLRLMNELYLKVPVYTDVDTLAYTLPRNSCPDLSMYRVEPAPISRKRAFVS 356
Db 322 TAEFKETRRRLS-----VEIYDKFQRAISV-----RRKLS- 351
Qy 357 CADMYGAOREAGMVHANSDDTLTKLDREKTFETABAYHOTDILAKVYNALATVVKPPAE 416
Db 352 -AELAG-----NINQELTPCRR-----TSLVNLHLS-----REVLPPLLK 386
Qy 417 QEDAAIYG 424
Db 387 ABSIYLYNG 394

RESULT 6
ID O95069 PRELIMINARY; PRT; 426 AA.
AC O95069; Q9UN63;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE
DE POTASSIUM CHANNEL TPCK1) (TREK-1 K+ CHANNEL SUBUNIT).
GN KCNK2 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
" Inhaled anesthetic activate two-pore-domain background K+
channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CHANNELS.
DR EMBL; AF129399; AAD47569.1; -.
DR EMBL; AF004711; AAD01203.1; -.
DR MIN; 603219; -.
DR INTERPRO; IPR000099; -.
DR INTERPRO; IPR001622; -.
DR PFAM; PF02034; TWIK_Channel; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
Glycoprotein; Phosphorylation.
FT DOMAIN 1 61 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 62 82 POTENTIAL.
FT DOMAIN 144 170 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 223 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 253 283 PORE-FORMING (BY SIMILARITY).
FT TRANSMEM 288 308 POTENTIAL.
FT DOMAIN 309 426 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
SENSITIVITY (BY SIMILARITY).
FT DOMAIN 354 426 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
SIMILARITY).
FT MOD_RES 38 38 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 315 315 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 318 318 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 343 343 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 348 348 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 360 360 PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 2 16 MISSING (IN REF. 2).
FT CONFLICT 309 311 RLV -> DML (IN REF. 2).
FT CONFLICT 391 391 S -> N (IN REF. 2).
FT CONFLICT 411 411 A -> T (IN REF. 2).
SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match
Best Local Similarity 9.0%; Score 295.5; DB 4; Length 426;
Matches 102; Conservative 76; Mismatches 168; Indels 65; Gaps 15;

Qy 9 LLFIYISYLMFGAALYYHIEGEEKISRAEQKQAIAINEYLLELGDKNNTTQDEILQR 68
Db 65 IFLVVVLYLIIGATVFKALEQPHE---ISQRTTIVIOKQTFISQSCVNSTELDELIOQ 120
Qy 69 ISDYCDKPVTLPTDDTPYTWTFYHFAFFAFTVCGTGVGNISPTTFAGRMIMTAYSVI 128
Db 121 IVAAINAGIILPLGNTSNQISHWDLGSSFFACTVTTTIGFNGNISPTTEGKIFCIYALL 180
Qy 129 GIPVNGILFAG-----LGEVFGRTFAIYRYKKYKMSDTHVVPQGLGLITTVIALIPG 184
Db 181 GIPLEFGLLAGVDQGLTIFGKIAKVEDTFIKNVS-----QTKIRIISTIIILF-G 233
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Qy	185	I A L F L V P C V G V H L L R E L - G L S S I - S L Y S Y V T T T I G F C D Y Y P T C A N Q K P E F G G W F V	242
Dd	234	C V L F E A L P A I - - - I F K H I E G S A L D A I F Y F V I L T T I G F G D Y V A - - - - - G G S D I E	280
Qy	243	Y O I F E V - - I V W F - - I F S L G Y L V M I M T F T I R G L Q - - S K L A Y L E Q L S S N L K A T Q N R I W S G	296
Dd	281	Y L D Y K P V W F W I L G L A Y A A V L S M L G R L V R V I S K - - - - - P K E E V G E F R A H A E W T A N V	336
Qy	297	T K D V G Y L R R M L N E L Y I L K V K P V Y T D V D I A Y T L P R S N C P D L S W Y R V E P A P I P S R K R A F S V	356
Dd	337	T A E F K E T R R R L S - - - - - V E I Y D K F Q R A T S I R K L S A E L A G N H N Q E L T P - - - - -	379
Qy	357	C A D V M G A Q R E A G W H A N S D F D L Y K - - L D R E K T F E T A E A V H Q T T D L L A K V V N	405
Dd	380	- - - - - C R R T L S V N H L T S E R D V P P L L K T E S I Y L N G L A P H C A G E E I A V I E N	424
RESULT	7		
ID	Q9JIS4	PRELIMINARY;	PRT; 538 AA.
AC	Q9JIS4;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DE	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)		
DE	POTASSIUM CHANNEL TREK-2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	{1}		
RA	SEQUENCE FROM N.A.		
RA	Bang H., Kim Y., Kim D.;		
RT	"TREK-2", a new member of the mechanosensitive tandem-pore K+ channel family.;		
RL	J. Biol. Chem. 275:17412-17419(2000).		
DR	EMBL; AF196965; AAF75132.1; .		
SO	SEQUENCE 538 AA; 59800 MW; 1FF33FOAA52B97E4 CRC64;		

Db	424	RLKGP	-----EQLNKHG--QGASEDNI-----INFGSTSKLTKRKNKDLKTLPE	467
Qy	467	-----RWQSERPLRSHNEWTSWGDQ---QIQEAFNQRYKGQQRANGAANSTWY	513	
Db	468	DVQKIYTFERNYSUDEEKKKDETEKMCNSDSSSTAMLTCEIQOO---ABEMENG----	MV 519	
Qy	514	HLEPDALAEELRN 527		
Db	520	PM--DTKDDGLENN 531		
RESULT	8			
Q9NRT2		PRELIMINARY; PRT; 411 AA.		
AC	Q9NRT2			
DT	01-OCT-2000 (TEMBLrel. 15, Created)			
DT	01-OCT-2000 (TEMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TEMBLrel. 15, Last annotation update)			
DE	TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.			
GN	TREK-1			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUP-BRAIN;			
RA	Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,			
RA	Medhurst A.J., Murdoch P., Chapman C.G.;			
RT	"Cloning, localization and functional expression of the human ortholog			
RT	of the TREK-1 potassium channel."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF171068; AAF89743.1;			
KW	Ionic channel.			
SO	SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;			
Query Match 8.9%; Score 292.5; DB 4: Length 411;				
Best Local Similarity 25.2%; Pred. No. 4e-15;				
Matches 108; Conservative 72; Mismatches 153; Indels 95; Gaps				
Qy	9	LLPIYSYLMFGAAIYHIEHGEEKISRABQRAQAINLEYLLEELGDKNNTTQDEILOR	68	
Db	50	IFLVVLYLIGATVFKALEQPEH-----ISQRTTIVIQKTFISQHSVCYNSTDELIIQ	105	
Qy	69	ISDYCDKPVTLPPYTDPTWTYTHFAFFAFTVCGSTVGNSIPSTTFAGRMIMTAYSVI	128	
Db	106	IVAINAGIPLGNTSNQISHWDLGSSFFAGVITTFGNSIPRTGEGKFCIYALL	165	
Qy	129	GIPVNGILFAG---LGEYGRTFEAIYRKYKYMSTDMHYVPPLGLTTTWTIALIPG	184	
Db	166	GIPLFGFLAGVGQDLGTIFGKGIKAVEDETFIKWNVS-----QTKIRIISTITILF-G	218	
Qy	185	IALLPLVPCGVHLLREL-GLSSI-SIYYSYVTTTIGFDYVPTPGANQKPEFGWFV	242	
Db	219	CVLVEALPAI---IFKHIEGWSALDAIFVVTITIGFDGYA-----GSDIE	265	
Qy	243	YQIEV---IVWF---IFSLGYLVMTITTRGLQ---SRKLALEYQQLSSNKLATQNRIWGSV	296	
Db	266	YLDYFKPVVFWIILVGLAYFAAVLSMIGDLRLVISKK---TKEEVEGFRAHAAEWTV	321	
Qy	297	TKDVGYLRLMLNELYLKVKPVYTDVDIAYTLPRNSCPDLSWMYVEPAPISRKAFSV	356	
Db	322	TAEPKPTRRRLS-----VEIYDKFORATSI-----RKRLS-	351	
Qy	357	CADMVGAQRAGMVHANSDDTLTKLDREKTFETAEAYHOTDILLAKVVALATVKPPPAE	416	
Db	352	-AELAG-----NHNQELTPCRR-----TSLVNHLTSE-----RDVLPPLLK	386	
Qy	417	QEDAAALYG 424		
Db	387	TESIYLVNG 394		


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RN [1]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Kunkel M.T., Wei A., Butler A., Salkoff L.;
RT "Analysis of genomic organization of nematode 4Tm potassium
   channels.";
RL Ann. N.Y. Acad. Sci. 0:0-0(1998).
DR EMBL: AF083645; AAC32856.1;
KW INTERPRO: IPR001622;
SQ SEQUENCE 555 AA; 63858 MW; 4D4E0787AEA3008C CRC64;

Query Match      8.1%; Score 264.5; DB 5; Length 555;
Best Local Similarity 23.3%; Pred. No. 1e-12;
Matches 151; Conservative 78; Mismatches 234; Indels 185; Gaps 33;

Qy 9 LLIFVSYLMFGAAYHYHIE---HGEKISRAEORAKQAIANEVLLLEL---GDKNTTTQD 63
Db 29 LLMVLVLSYFGGFIDRIETNAHAEMKRNERINTACVS---QILHSIHRWSNQTHKV 85
Qy 64 EILQRISDYCDKPVTLPTPTDYTFYHAFFFAFTVCSVGYGNISPTTFAGRMIMI 123
Db 86 QYAEADIAD-CFEP-----EKDERSENFTVATLYGFGIVTTLGYNRIAPITYTGRMFCI 138
Qy 124 AYSVIGIPVNGILFAGLGEYFG-----RTFEAIYRYKK-----YKMTDMHY 166
Db 139 VYGICGIPVTMIITANVQYLLNFAAGSRKKIEA-YRQORMSKASLAGKTYKESS---- 193
Qy 167 VPPQGLITTVVIALIPGIALFVLPVCGVHLL-----RELGLSSISLYSVVTTTIGFG 222
Db 194 -----IQVTSAL---LCVFLYIVAVGALLPLLNGLDFFN-GLYFNFLCLTAIDFG 242
Qy 223 DYVTFGANQKRGFGVVFVYVIMVIFSLGYLVNIMTFITRGLQSKRLAYLEQOLS 282
Db 243 QLVP-----IRVELLPITFLYVCIGLATTIATNIGSEVMKKLHWGKKMK 288
Qy 283 SNLKATONRIWSGVTKDGYLRMLNELYLKVKPVTVTDVIAITLPRNSCPDLSMYRV 342
Db 289 N---AAQTRIFGFGK-----TLKVR-----DLLHAV--GKKC-----GV 317
Qy 343 EPAPISPKRAFSVCADWGAQREAGMVHANSDTLTKLDREKTFETAAYVHQTDLAK 402
Db 318 EP-----GMIDA---LQLENV-VERTIAMQEGREPPELDNDE 350
Qy 403 VVNALATVKPPAPQEDAAALGYGHGFSQSLASEMSFSTVNEFTSPRRPRACRACSDFN 462
Db 351 -----PPREP-----SPRSIIHSPCSTRPSNPPMSPSPREDHPHFIFK 388
Qy 463 LEAPWQSERPL-----RSSHNEWTSQDNGQIQE-AFNQRYKQQRAN----- 505
Db 389 MDAPAPRSLPLPAYELDIKKPIQALSNEFM-----NOSAQEKLFNDLDTFQIEINTELV 444
Qy 506 -GAANSTMVHLEDALEQLRNHRVPV-----ASRSSPCRMVCDVCFPSRRS-----TPRR 556
Db 445 EDHKCESVIIIEPPATFEDMTIQHSLSLCEVDEYEREEKVPKR-----FREKKEMYGRDPRK 498
Qy 557 IWSA-SCPWSRYPRVSRKRPDPRTWTTSTRSRPPVNPICATDAVRH 603
Db 499 LYETYQEWDLERLSD-RKHGPRKRVSLNLSNCSPPSV-SPSPIRH 544

RESULT 12
Q9XU07 PRELIMINARY; PRT; 393 AA.
AC Q9XU07
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE T28A8.1 PROTEIN.
GN T28A8.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
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OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94150718; PubMed=7906398;
RL Lloyd C.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
   elegans.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton A., Dear Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lighning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
   elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z92813; CAB07286.1;
DR INTERPRO: IPR001622;
SQ SEQUENCE 393 AA; 45125 MW; C02BE5ED022EBD8 CRC64;

Query Match      8.0%; Score 264; DB 5; Length 393;
Best Local Similarity 24.4%; Pred. No. 6.9e-13;
Matches 75; Conservative 58; Mismatches 120; Indels 54; Gaps 9;

Qy 7 ILLLIFFVSYLMFGAAYHYHIECEE-----KISRAEORAKQI-----ATNEYL 50
Db 15 VSLVLVSVTVGGAFLFYQLEQFNEVEVRARNIERNIHKROMIEHLWEMRESGIGQHV 74
Qy 51 LEELGDKNTTTQDEIL-QRISDYCDKPVTLPTPTDYTFYHAFFFAFTVCSVGYG 109
Db 75 VEDLAVKYVDNVTRILPEAFDTHCIGAKHLRPGGDEEDYNWYMTALFFTTLLTTIGY 134
Qy 110 NISPTTFAGRMIMAYSVIGIPVNGILFAGLGEYFGTFEAIYRYKKYK----- 159
Db 135 NLTPVTGRGKLLCILYALFGVPLITVADIGKFLSENIVOLYTWYRKLREKSKQKYSV 194
Qy 160 -MSTDMHYVPPQLGL-----ITTVVIALIPGIAL-FLVLPVCGVHLLRELGLSSISLYS 212
Db 195 ISSKDDKNKEGDLNLDHLENYISIPILVAILLSYITFGAVVLSMWEGWDFTS-GEYFS 253
Qy 213 YVTTTITGFGDYVPTFGANQKRGFGVVFVYVIMVIFSLGYLVNIMTFITRGLQSK 272
Db 254 FIWTVTGFQDVLPL-----KREY-----YILDLCYIIIGLSITTCIDLV 294
Qy 273 KLAYLEQ 279
Db 295 GIOYIRK 301

RESULT 13
Q9Z2T2 PRELIMINARY; PRT; 336 AA.
ID Q9Z2T2
AC Q9Z2T2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE POTASSIUM CHANNEL TWIK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
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RA Kaczmarek L.K.;
RT "Cloning and localization of rTWIK, a putative potassium channel with
two P domains."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF022819; AAD09336.1; -
DR INTERPRO: IPR000099; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR001779; -
DR PFAM: PF02034; TWIK_channel; 1.
DR PRINTS: PR01096; TWIK1CHANNEL.
DR PRINTS: PR01333; 2PORECHANNEL.
KW Ionic channel.
SQ SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 7.7%; Score 251.5; DB 11; Length 336;
Best Local Similarity 25.7%; Pred. No. 5.4e-12;
Matches 84; Conservative 65; Mismatches 143; Indels 35; Gaps 11;

QY 9 LLIFVSYLMFGAAYIYHIEGEEKISRAEQKAKAIANEYLLEELGDKNTTQDEILOR 68
Db 26 LVLGVLVLFVGAIVFSSVEPYEDLLQELRK----LKRREHECLSEPLEQFLGR 81
QY 69 ISDYCDKPVTLPTDDPTTFTFTHAFPAFTVCGTGYGNISPTTAPGRMIMIAYSVI 128
Db 82 VLEASNYGVSVLSNAGN-WNWDFTSALFFASTVLTGTGYGHVPLSDGGRKAFCIYVI 140
QY 129 GIPVANGILFAGLGEYFGRTFEAIYRYRYKMKSTDMHYVPPQLG---ITTVVIALIPO- 184
Db 141 GIPFT-LLF-----LTAVQRTVHVTRRPVLFHIRWGFSKQVVAIVHAVLLGF 189
QY 185 --IAFLVLPVGVHLLRELGLSSISLYSYVTTTTIGDGVVPTFGANQPKFEGWV 242
Db 190 VTVSFFFTPAAVFVLEDDWNFLSEYFCFTSLTIGLDYVPGEGYNQK----FREL 244
QY 243 YQIVVWVFISL-GYLVNMF--ITRGLOSKKLAYLEQQLSS---NLKATQNRITWGV 296
Db 245 YKIGITCYLLGLAMLVNLETFCEHLKFKRMFYVKKDKDEQVHMEHQDLSFSSI 304
QY 297 TKDVGYLRL--RMLNELYLKVPVYT 321
Db 305 TEOAGLKEEQKNEFFVASQSPYED 331

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O17935 PRELIMINARY; PRT; 523 AA.
AC O17935; 045977;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE K06B4.12 PROTEIN.
GN K06B4.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
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RA Lloyd C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z83233; CAB05769.1; -
DR EMBL: AL021175; CAB05769.1; JOINED.
DR EMBL: AL021175; CAA15972.1; -
DR EMBL: Z83233; CAA15972.1; JOINED.
DR INTERPRO: IPR001622; -
DR PRINTS: PR01333; 2PORECHANNEL.
SQ SEQUENCE 523 AA; 59598 MW; 8A0286680561AC48 CRC64;

Query Match 7.5%; Score 247; DB 5; Length 523;
Best Local Similarity 20.8%; Pred. No. 2.3e-11;
Matches 100; Conservative 88; Mismatches 161; Indels 132; Gaps 19;

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Db 188 TTTTAEAMQVYIREAVVSLMKLEGQYKGYKLEDHGKNWKTFFESAFFFSMNVYTTG 247
QY 108 YGNISPTTFAGRMIMIAYSVIGIPVNGILFAGLGEYF---GRTFEAIYRYRYKMKMSTD 163
Db 248 YGSIAPESILGVVLCYGFIFVPTVLTALRDIGQFVLVHLTKLYAQLIQRWREINGDTS 307
QY 164 MHYVPPQLGIITVTIALIPGIALFLVPCVGVHLLREL-----GLS-SISLYYSYVT 215
Db 308 IDVNE-----IIKIPKACILLALLALYAFCTFIHVFDELSGDSGSMVFICFYFSFIS 363
QY 216 TTTTIGDGVVPTFGANQPKFEGWVYQIFVIVWFIISLGYLVNMTITFITRGLQSKLA 275
Db 364 LSTIGLDIMPNNATFSP-----IISIMFFGMA-----LTKVNVNRTFI 403
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Db 404 AVENGIFGALTIVENKL-DGIVR-----KQKEMP 431
QY 336 DLSMYRVEPAIPSR--KRAFSVCAADMVGAQREAGMVHANSDDTLKLDREKTFETAAY 393
Db 432 D---EOKQPKALTPQMIQRLSV-EDYGAQRENKNEVMNFT-----470
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DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1.
GN KCNK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Date: Mar 17, 2001 7:23 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Sequence					
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gb_in3:DMU55321	+ 3165.50	2488.36	1.9e-130	3568	I26670 Sequence 1 from patent
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gb_in1:AE003484	- 2648.00	2052.01	3.9e-106	314087	I26670 Sequence 1 from patent
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gb_ro:AF056492	+ 312.00	254.08	5.4e-06	1795	I26670 Sequence 1 from patent
gb_ro:AF259395	+ 310.00	253.68	5.7e-06	1509	I26670 Sequence 1 from patent
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gb_pr4:AF279890	+ 300.00	241.82	2.6e-05	2730	I26670 Sequence 1 from patent
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VERSION	I26670.1	GI:1606540			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2441)				
AUTHORS	Price L.A. and Pausch M.H.				
TITLE	Genes encoding a novel family of potassium channels				
JOURNAL	Patent: US 5559026-A 1 24-SEP-1996;				
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DEFINITION mRNA, complete cds.
ACCESSION U55321
VERSION U55321.1 GI:3808067
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 3568)
AUTHORS Goldstein,S.A., Price,L.A., Rosenthal,D.N. and Pausch,M.H.
TITLE ORK1, a potassium-selective leak channel with two pore domains
cloned from Drosophila melanogaster by expression in Saccharomyces
cerevisiae
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (23), 13256-13261 (1996)
MEDLINE 97075152
REFERENCE 2 (bases 1 to 3568)
AUTHORS Goldstein,S.A.N., Price,L.A., Rosenthal,D.N. and Pausch,M.H.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1996) S.A.N. Goldstein, Pediatrics and Cellular
and Molecular Physiology, Yale University School of Medicine, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA
REFERENCE 3 (bases 1 to 3568)

AUTHORS Goldstein, S.A.N., Price, L.A., Rosenthal, D.N. and Pausch, M.H.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1998) S.A.N. Goldstein, Pediatrics and Cellular
and Molecular Physiology, Yale University School of Medicine, Boyer
Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
06536, USA

REMARK Sequence update by submitter
COMMENT On Oct 29, 1998 this sequence version replaced gi:1666502.

FEATURES

Location/Qualifiers
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ORIGIN

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Ratio: 5.147 Gaps: 3

Percent Similarity: 99.194 Percent Identity: 97.903

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ACCESSION  AC013909
VERSION    AC013909.1  GI:6437426
KEYWORDS   HTG; HTGS_PHASE2.
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              Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 21163)
AUTHORS      Adams,M. and Venter,J.C.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
              Rockville, MD, USA
COMMENT      This sequence was identified as CDM:10210421 by the submitter.
              For further information on this sequence e-mail to fly@celera.com.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
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DEFINITION Drosophila melanogaster genomic scaffold 142000013386053 section 1
of 30, complete sequence.

ACCESSION AE003484 AE002593
VERSION AE003484.1 GI:7292554
KEYWORDS HTG.

SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 314087)
Adams,M.D., Celisner,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galie,R.F.,
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Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

Direct Submission

TITLE

JOURNAL

Location/Qualifiers

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DEFINITION Mus musculus potassium channel TASK2 mRNA, complete cds.

ACCESSION AF259395

VERSION AF259395.1 GI:7717038

KEYWORDS house mouse.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 1509)

Roux, J. and Barhanin, J.

Mouse two P domain potassium channel TASK2

Unpublished

2 (bases 1 to 1509)

Roux, J. and Barhanin, J.

Direct Submission

Submitted (20-APR-2000) IPMC, CNRS, 660, Route des Lucioles,

Valbonne 06560, France

FEATURES

source

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DEFINITION Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds

ACCESSION AF084830

VERSION AF084830.1 GI:3925426

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 3514)
Reyes,R., Duprat,F., Lesage,F., Fink,M., Salinas,M., Farman,N. and Lazdunski,M.

TITLE

Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney

J. Biol. Chem. 273 (47), 30863-30869 (1998)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

2 (bases 1 to 3514)
Reyes,R., Duprat,F., Lesage,F., Fink,M., Salinas,M., Farman,N. and Lazdunski,M.

TITLE

Direct Submission

JOURNAL

Submitted (17-AUG-1998) IPCM, CNRS, 660 Route des Lucioles, Sophia Antipolis, Valbonne 06560, France

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DEFINITION Mus musculus TREK-1 K+ channel subunit mRNA, complete cds.
ACCESSION U73488
VERSION U73488.2 GI:4584798
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3580)
AUTHORS Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and Lazdunski,M.
TITLE Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel
JOURNAL EMBO J. 15 (24), 6854-6862 (1996)
MEDLINE 97157476
REFERENCE 2 (bases 1 to 3580)
AUTHORS Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and Lazdunski,M.
TITLE Direct Submision
JOURNAL Submitted (07-OCT-1996) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France
REFERENCE 3 (bases 1 to 3580)
AUTHORS Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and Lazdunski,M.
TITLE Direct Submision
JOURNAL Submitted (15-APR-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France
REMARK Sequence update by submitter
COMMENT On Apr 15, 1999 this sequence version replaced gi:1794281.
FEATURES Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1993)
Fink M., Honore E., Duprat F., Lesage F. and Lazdunski M.
Novel mechanosensitive mammal potassium channel family
activated by polyunsaturated fatty acids and their use particularly
for screening medicines
Patent: WO 9945108-A 10-SEP-1999;
FINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE
FLORIAN (FR); CENTRE NAT RECH SCIENT (FR); LAZDUNSKI MICHEL (FR)

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LOCUS AX003051 1994 bp DNA ROD 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9937762.
ACCESSION AX003051
VERSION AX003051.1 GI:9926936
KEYWORDS house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1994)
AUTHORS Chapman,C.G. and Meadows,H.J.
TITLE Trek-1 like two pore potassium channel
JOURNAL Patent: WO 9937762-A 29-JUL-1999;
SMITHKLINE BEECHAM PLC (GB)
FEATURES Location/Qualifiers
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BASE COUNT 426 a 561 c 561 g 446 t
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Quality: 298.50 Length: 316
Ratio: 1.588 Gaps: 13
Percent Similarity: 59.494 Percent Identity: 28.481


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DEFINITION Rattus norvegicus potassium channel TREK-2 mRNA, complete cds.
ACCESSION AF196965
VERSION AF196965.1 GI:8452899
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1854)
AUTHORS Bang,H., Kim,X. and Kim,D.
TITLE TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
JOURNAL J. Biol. Chem. 275 (23), 17412-17419 (2000)
MEDLINE 20298807
REFERENCE 2 (bases 1 to 1854)
AUTHORS Kim,D. and Bang,H.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Physiology and Biophysics, Finch University
of Health Sciences/The Chicago Medical School, 3333 Green Bay Road,
North Chicago, IL 60064, USA
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371 isAlaAsnSerAspThrAspLeuThrLysLeuAspArgGluLysThrPhe 387
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seq_documentation_block:

LOCUS AF004711 2106 bp mRNA PRI 05-JAN-1999
DEFINITION Homo sapiens two-pore potassium channel TPKC1 mRNA, complete cds.

ACCESSION AF004711

VERSION AF004711.1 GI:4101565

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2106)

AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.

JOURNAL TPKC1

Unpublished

REFERENCE 2 (bases 1 to 2106)

AUTHORS Price,L.A., Hellings,S.E., Hayashi,J.H. and Pausch,M.H.

TITLE Direct Submission

JOURNAL Submitted (19-MAY-1997) Cyanamid Agricultural Research Center,

American Cyanamid Company, PO Box 400, Princeton, NJ 08543-0400.

USA

FEATURES

source Location/Qualifiers

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BASE COUNT 552 a 471 c 486 g 581 t 16 others

ORIGIN

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Quality: 295.50 Length: 411

Ratio: 1.296 Gaps: 15

Percent Similarity: 55.474 Percent Identity: 24.818

alignment_block:

US-08-816-011C-2 x AF004711 ..

Align seg 1/1 to: AF004711 from: 1 to: 2106

9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25

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346 ATATTCCTGGTGGTTGCTCTATCTGATCATCGGAGCCACCGGTGTCAA 395

25 rHisIleGluHisGlyGluGlyLysIleSerArgAlaGluGlnArgLysA 42

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396 AGCATTTGGAGCAGCCTCATGAG.....ATTTCACAGAGGACCA 433

42 lagIleIleAlaIleAsnGluTyrLeuGluLeuGlyAspLysAsn 58

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OM of: US-08-816-011c-2 to: N_Geneseq_36:* out_format : pfs

Date: Mar 17, 2001 7:55 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US08816011/runat_07302001_122539_23551/app_query.fasta_1.686
-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-FGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=BIOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
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Search information block:

Query: US-08-816-011c-2

Query length: 618

Database: N_Geneseq_36:*

Database sequences: 480022

Database length: 187831343

Search time (sec): 90.290000

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ID T33201 standard; cDNA; 2441 BP.

XX AC T33201;

XX DT 16-OCT-1996 (first entry)

XX DE DmORF1 potassium channel gene.

XX KW DmORF1; potassium channel; fruitfly; polyadenylation site;

XX KW potassium dependence; Saccharomyces cerevisiae; potassium-agonist;

XX KW potassium-antagonist; drug screening; insecticide; cardiac disorder;

XX KW ss.

XX OS Drosophila melanogaster.

XX FH Key Location/Qualifiers

XX FT CDS 190..2046

XX FT /*tag= a

XX FT /product= Potassium channel DmORF1 protein

XX FT polyA_signal 2093..2098

XX FT /*tag= b

XX PN W09613520-A1.

XX PD 09-MAY-1996.

XX PF 25-OCT-1995; 95WO-US14364.

XX PR 31-OCT-1994; 94US-0332312.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Pausch MH, Price LA;

XX DR WPI; 1996-239450/24.

XX DR P-PSDB; R97984.

XX PT Potassium channel genes from Drosophila melanogaster and

XX PT Caenorhabditis elegans - useful in assaying substances to determine

XX PT effects on cell growth, and in inhibiting nematode and insect pests

XX PS Claim 11; Page 34-37; 79pp; English.

XX CC The sequence encodes potassium channel DmORF1 protein from

XX CC Drosophila melanogaster, with 2 pore-forming domains between

XX CC transmembrane helix domains. The sequence has been isolated by

XX CC complementation of the potassium-dependent phenotype of

XX CC Saccharomyces cerevisiae Cvi62 (trk1-delta) on low-potassium medium.

XX CC The 5'-untranslated sequence contains long poly-A and poly-T tracts

XX CC not likely to be found in protein coding regions. A consensus

XX CC polyadenylation site is found in the 3'-untranslated sequence.

XX CC Primers T33205-06 may be used to amplify the open reading frame, for

XX CC cloning and expression in Xenopus laevis oocytes and assaying

XX CC induced potassium currents. The DNA may be inserted in a vector

XX CC and expressed in a host cell to assay substances to determine

XX CC effects on cell growth. Potassium-agonists or potassium-

XX CC antagonists identified by this method may be used as insecticides

XX CC or in therapy of cardiac disorders, etc.

XX SQ Sequence 2441 BP; 555 A; 702 C; 665 G; 519 T; 0 other;

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Ratio: 5.312 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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67 nArgIleSerAspTyrCysAspLysProValThrLeuProThrTyrA 84
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567 rProArgValSerSerArgArgLysProAspProArgTrpThrThrThrs 584

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295 y.....ValThrLys.AspValGlyTyrLeuArgArgMet 306
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1176 CAGAGA..... 1181

323 pLeaAlaTyrThrLeuProArgSerAsn...SerCysProAspLeuSerM 339
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339 etTyrArgVal.....GluProAlaProIlePro 348
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349 SerArgLysArg 352
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PA (PROT-) PROTEGENE INC.

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87 roTyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCys 103
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120 tIleMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuP 137
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1006 .GCCAACTACCACGCGCTGTACCGTACTCTGTGGAGCTCTGTGATCTAC 1053
253 PheSerLeuGlyTyrLeuValMetIleMetThrPhe..... 264
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1054 TTGGGCTGGCTGGCTGTCTCTCTCTTTTGTCACTGGAAGGTGAGCATGTT 1103
265 .....IleThrArgGlyLeuGlnSerTyrLysLeuAlaTyrLeuGluG 279
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1104 TGTGGAAGTCCACAAGCCATTAAAGAGCGCGCGCGAGGAGT 1153
279 InGlnLeuSerSer.....AsnLeuLysAlaThrGlnAsnArgIleTrp 293
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1154 CTTTGTGAGAGCTCCCACTCCCGAAGGCGCTGTGAGTGAAG...GGG 1200
294 SerGlyValThrLysValGlyTyrLeuArgArgMetLeuAsnGluLe 310
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1201 AGCAGAGCTTCAAGGACGTCACATCTTCAGC..... 1233
310 uTyrIleLeuLysValLysProValTyrThrAspVal.....AspIleA 325
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1234 .TTTCTTTCAAGAGAACAGACCTACACGACCTCATCAACGACGATCG 1282
325 laTyrThrLeu..... 328
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1283 GGAAGAAGGCGCATGAGACAAGCGGGGTGGGAGAGCGGCCCGGCCCA 1332
329 .....ProArgSerAsnSerCysProAspLeuSerMetTyrArgVa 342
||||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1333 GGCTGGGCGCTCAAGGCGGTGGCTCCCAAGCAGCTGCCCTTCCCTGGT 1382
```

```
342 lGluProAlaProIleProSerArgLysArgAlaPheSerValCysAlaA 359
| ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1383 G...CCCTGGTAGTCTACTTCCAAAGAACCGGGTG...CCACCTTGGGAAG 1426
359 sPmetValGlyAlaGlnArgGluAlaGlyMetValHisAlaAsnSerAsp 375
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1427 AGGTGTACAGACACTGAGGAGCAAGGCGACGATATCAAGTCCCCAGAT 1476
376 ThrAspLeuThrLysLeuAspArgGluLysThrPheGluThrAlaGluAl 392
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1477 GAGAGGCTGTGGCAGGCGCCCTGAGACAGCTCCCTGCCCGCCGAGGT 1526
392 aTyrHisGlnThrThrAspLeuLeuAlaLysValValAsnAlaLeuAla 409
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1527 GTTCATGAACACGAGCTGAGCGCATCAGCGAG..... 1557
409 hrValLysProProAlaGluGlnGluAspAlaAlaLeuTyrGlyGly 425
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1558 ....GAATGCGAGCATGGGACGCCGAGGAC..... 1584
426 TyrHisGly.....PheSerAspSerGlnIleLeuAlaSerGluTrpSe 440
||||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1585 TACCACCCACTCATCTTCCAGGAGCGCAGATCACCTTCTGTGACACCGGA 1634
440 rPheSerThrValAsnGluPheThrSerProArgArgProArgAlaArgA 457
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1635 GGCTGGCTCTCAGACGAGGAGACCTCC.....AAGT 1666
457 laCysSerAspPheAsnLeu.....GluAlaProArgTrp..... 468
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1667 CTTCTGATAGGAGCAACTTGGCAGGAGGAGAGAGCCCGCAGGAGGGCT 1716
469 GlnSerGluArgProLeuArg.....SerSerHisAsnGluTr 481
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1717 GAGCCAAAGCGCCCTTGAACATGGGGAGTTCCTCTCTCTCCCGAGTC 1766
481 pThrTrpSerGlyAspAsnGlnGlnIleGlnGluAlaPheAsnGlnArgT 498
||||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1767 CACCTTACCAGCAGCTCAGTCTGAGCTCTGTCTGTCTTACGACAGCTGA 1816
498 yrlYsGlyGlnGlnArgAlaAsnGlyAlaAlaAsnSerThrMetValHis 514
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1817 TGAATGAGTACAAAGGCTTAACAGGCCCAAGG.....CAC 1853
515 LeuGluProAspAlaLeuGluGlnLeuArgAsnAsnHisArgValPr 531
: : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1854 ATGAGCAGGCGCGCTCCCT.....ACCC 1879
531 oValAlaSerArgSerSerProCysArgMetValCysAspValCysPheP 548
| ||| ||| : : : ||| : : : ||| : : : ||| : : : |||
1880 ACCTTTGATGGCTCTTCCCGCTCACCCTAGGGTGT.....C 1917
548 roSerArgArgSerThrProArgIleTrpSerAlaSer 561
||||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1918 CCGAGATGACCGGAGCGCTGGCCCTGGTGGGGGGGCGAGC 1958
```

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/Nx2000.DAT:AL15943

seq_documentation_block:

ID AL15943 standard; cDNA; 1497 BP.

XX AC AL15943;

XX DT 12-JUN-2000 (first entry)

XX DE Human protein clone HP10538 coding sequence.

XX KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;

XX KW cytokine production; cell proliferation; cell differentiation;

XX KW immune deficiency; infectious disease; autoimmune disorder; asthma;

XX KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;

XX KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;

nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; systemic cytokine damage; tissue differentiation; reperfusion injury; stroke; coagulation disorder; myocardial infarction; inflammatory condition; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour; nephritis; therapy; ss.

Homo sapiens.

WO200005367-A2.

03-FEB-2000.

22-JUL-1999; 99MO-JP03929.

24-JUL-1998; 98JP-0208820.

07-AUG-1998; 98JP-0224105.

25-AUG-1998; 98JP-0238116.

09-SEP-1998; 98JP-0254736.

29-SEP-1998; 98JP-0275505.

(SAGA) SAGAMI CHEM RES CENT.
(PROT-) PROTEGENE INC.

Kato S, Kimura T;

WPI; 2000-182694/16.

P-PSDB; Y94875.

Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -

Claim 3; Page 252-253; 351pp; English.

This sequence encodes a human protein of the invention, which has hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of haematopoiesis and consequently in the treatment of myeloid or lymphoid cell deficiencies. It is also used in compositions for tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activin or inhibin related activities and as a fertility inducing therapeutic. They are used for treating various coagulation disorders and in treatment and prevention of conditions resulting from coagulation activities e.g. myocardial infarction or stroke. They also acts as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to prevent tumours.

Sequence 1497 BP; 328 A; 447 C; 438 G; 284 T; 0 other;

alignment_scores:

Quality:	301.00	Length:	541
Ratio:	1.020	Gaps:	23
Percent Similarity:	54.529	Percent Identity:	24.584

alignment_block:

US-08-816-011c-2 x A15943

Align seg 1/1 to: A15943 from: 1 to: 1497

```

4 AsnArgTrpIleLeuLeuLeuIlePheTyrIleSerTyrLeuMetPheG1 20
  ::::: ||||| ||| ||||| :::::
7 GACGGGGCCCTGCTGCATCCATCGGCCATCTTCTACCTGGCCATCGG 56
  ::::: ||||| :::::
20 YAlAlAlIleTyrTyrHisIleGluHisGlyGluGluLysIleSerArgA 37
  ||||| ||||| ::::: ||||| ::::: |||||
57 GCGGGGATCTTCGAAGTCTGGAGGAGCCACACTGGGAG..... 96
  ||||| ||||| ::::: ||||| ::::: |||||
37 laGluGlnArgLysAlaGlnIleAlaIleAsnGluTyrLeuLeuGluGlu 53
  ||| ::::: ||||| ||||| ::::: |||||
97 ..GAGGCCAAGAAAACTACTACACACAGAAGTGCATCTCTCAAGGAG 144
  ::::: ||||| ::::: |||||
54 LeuGlyAspLysAsnThrThrThrGlnAspGluIleLeuGlnArgIleSe 70
  ::::: ||||| ||||| ||||| ::::: |||||
145 TTCCTGCTGCTGCTGAGGAGGCTGGACAAGATCTTAGAGTGGTATC 194
  ||||| ||||| ::::: |||||
70 rAspTyrCysAspLysProValThrLeuProProThrThrThrAspThrP 87
  ||||| ::::: ||||| ||||| ||||| ::::: |||||
195 TCATGCTGCAGCAGGAGGTGGCCATC.....ACAGGGAACACAGACCT 238
  ||||| ||||| ::::: |||||
87 rOTyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCys 103
  ::::: ||||| ::::: ||||| |||||
239 TCAACAACCTGGAACCTGCCCCAATGCAATGATTTTGCAGCAGCCCTCAT 288
  ||||| ||||| ::::: |||||
104 SerThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMe 120.
  ::::: ||||| ||||| ||||| ||||| ::::: |||||
289 ACCACCATGATGATGCAATGTGGCTCCCAAGAGACCCCGCGCTCGCT 338
  ||||| ||||| ::::: |||||
120 tIleMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeup 137
  ::::: ||||| ||||| ||||| ||||| ::::: |||||
339 CTTCTGCTGTTTCTATGGTCTCTCGGGGTCCCGCTGCTGCTGAGTGA 388
  ::::: ||||| ||||| |||||
137 heAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 153
  ::::: ||||| ||||| |||||
389 TCAGTGCCTGGCAAGTCTCTCGG.....GGA 417
  ||||| ||||| ::::: |||||
154 ArgTyrLysLysTyrLysMetSerThrAspMetHisTyrValProG1 170
  ||||| ||||| ::::: |||||
418 CGTCCCAAGAGACTAGGCGAGTCTCTTACCAAGAGAGGTGTGAGTCTGCG 467
  ||||| ||||| ::::: |||||
170 nLeuGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaL 187
  ::::: ||||| ||||| ||||| ||||| ::::: |||||
468 GAAGGCCAGATCAGTGCACAGTCTCTTTCATCGTGGGGCGCTCCTAG 517
  ||||| ||||| ::::: |||||
187 euPheLeuValLeuProCysValGlyValHisLeuLeuArgGluLeuGly 203
  ||||| ||||| ||||| ||||| ::::: |||||
518 TCCACCTGGTGTATCCCACTTC...GTATTCACTGGTACTGAG...GGG 561
  ||||| ||||| ::::: |||||
204 LeuSerIle....SerLeuTyrTyrSerTyrValThrThrThrI1 219
  ::::: ||||| ||||| ||||| ||||| ::::: |||||
562 TGGAGCTACATCGAGGCGCTCTACTCTCTCTCATCACCATCTCCACCAT 611
  ||||| ||||| ::::: |||||
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
  ||||| ||||| ||||| ||||| ::::: |||||
612 CGGCTTCGGTGACTTGTGGCC.....GGTGTGAACCCAGC..... 648
  ||||| ||||| ::::: |||||
236 heGlyGlyTrpPhePheValIleValIleValIleValIleValIle 252
  ::::: ||||| ::::: ||||| |||||
649 ..GCCAACTACCGCCCTGTACCGCTACTTCGTGGAGCTCTGACTCTAC 696
  ::::: ||||| ::::: |||||
253 PheSerLeuGlyTyrLeuValMetIleMetThrPhe..... 264
  ::::: ||||| ::::: |||||
697 TTGGGCTGCGCTGCTGCTCTCTTTTGTCAACTGGAAGGTGAGCATGTT 746
  ::::: ||||| ::::: |||||

```

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265 .....IleThrArgGlyLeuGlnSerLysLysLeuAlaTyrLeuGluG 279
    : : : : : : : : : : : : : : : : : : : : : : : :
747 TGTGGAAGTCCCAAGCCATTAAAGCGGGCGCGGCGGCGAGGAGT 796
    : : : : : : : : : : : : : : : : : : : : : : : :
279 InGlnLeuSerSer.....AsnLeuLysAlaThrGlnAsnArgIleTrp 293
    : : : : : : : : : : : : : : : : : : : : : : : :
797 CCTTTGAGAGCTCCCCACACTCCCGAAGCGCTGCAGCTGAAG...GGG 843
    : : : : : : : : : : : : : : : : : : : : : : : :
294 SerGlyValThrLysAspValGlyTyrLeuArgArgMetLeuAsnGluLe 310
    : : : : : : : : : : : : : : : : : : : : : : : :
844 AGCAGACGCTCCAGGACGCTCAACATCTTCAGC..... 876
    : : : : : : : : : : : : : : : : : : : : : : : :
310 uTyrIleLeuLysValLysProValTyrThrAspVal.....AspIleA 325
    : : : : : : : : : : : : : : : : : : : : : : : :
877 .TTTCTTTCGAAGAGGAAGACCTACACAGCCTCATCAAGCAGATCG 925
    : : : : : : : : : : : : : : : : : : : : : : : :
325 IaTyrThrLeu..... 328
    : : : : : : : : : : : : : : : : : : : : : : : :
926 GGAAGAAGGCCATGAAGACAAGCGGGGTGGGAGACGGCGCGGCCCA 975
    : : : : : : : : : : : : : : : : : : : : : : : :
329 .....ProArgSerAsnSerCysProAspLeuSerMetTyrArgVa 342
    : : : : : : : : : : : : : : : : : : : : : : : :
976 GGGCTGGGCGCTCAAGCGCGTGGCTCCAGCAGCTGCCCTTCCCTGCT 1025
    : : : : : : : : : : : : : : : : : : : : : : : :
342 IGLuProAlaProIleProSerArgLysArgAlaPheSerValCysAlaA 359
    : : : : : : : : : : : : : : : : : : : : : : : :
1026 G...CCCTGGTAGTCTACTCCAAGAACCGGGTG...CCACGCTTGAAG 1069
    : : : : : : : : : : : : : : : : : : : : : : : :
359 sPMetValGlyAlaGlnArgGluAlaGlyMetValHisAlaAsnSerAsp 375
    : : : : : : : : : : : : : : : : : : : : : : : :
1070 AGGTGTACAGACTGAGGAGCAAGGCGACGATATCAAGTCCCCAGAT 1119
    : : : : : : : : : : : : : : : : : : : : : : : :
376 ThrAspLeuThrLysLeuAspArgGluLysThrPheGluThrAlaGluAl 392
    : : : : : : : : : : : : : : : : : : : : : : : :
1120 GAGGAGGCTGTGGCAGGCGCCCTGAAGACAGCTCCCTGCCCCGAGCT 1169
    : : : : : : : : : : : : : : : : : : : : : : : :
392 aTyrHisGlnThrThrAspLeuLeuAlaLysValValAsnAlaLeuAlaT 409
    : : : : : : : : : : : : : : : : : : : : : : : :
1170 GTTCATGAACAGCTGGACCGCATCAGCGAG..... 1200
    : : : : : : : : : : : : : : : : : : : : : : : :
409 hrValLysProProProAlaGluGlnGluAspAlaAlaLeuTyrGlyGly 425
    : : : : : : : : : : : : : : : : : : : : : : : :
1201 .....GAATGCGGCGCATGGGAGCGGCCAGGAC..... 1227
    : : : : : : : : : : : : : : : : : : : : : : : :
426 TyrHisGly.....PheSerAspSerGlnIleLeuAlaSerGluTrpSe 440
    : : : : : : : : : : : : : : : : : : : : : : : :
1228 TACCACCCACTCATCTTCCAGGAGCGCCACATCCTTCGTGAACACGGA 1277
    : : : : : : : : : : : : : : : : : : : : : : : :
440 rPheSerThrValAsnGluPheThrSerProArgArgProArgAlaArgA 457
    : : : : : : : : : : : : : : : : : : : : : : : :
1278 GGCTGGCTCTCTCAGACGAGGAGACCTCC.....AAGT 1309
    : : : : : : : : : : : : : : : : : : : : : : : :
457 IaCysSerAspPheAsnLeu.....GluAlaProArgTrp..... 468
    : : : : : : : : : : : : : : : : : : : : : : : :
1310 CCTCGCTAGAGACAACTTGGCAGGGAGGAGAGCCCGCAGCGGGGCT 1359
    : : : : : : : : : : : : : : : : : : : : : : : :
469 GlnSerGluArgProLeuArg.....SerSerHisAsnGluTrp 481
    : : : : : : : : : : : : : : : : : : : : : : : :
1360 GAAGCCAAAGCGCCCTGAACATGGCGAGTTCCTCTCTCTCCGAGTC 1409
    : : : : : : : : : : : : : : : : : : : : : : : :
481 pThrTrpSerGlyAspAsnGlnGlnIleGlnAlaPheAsnGlnArgT 498
    : : : : : : : : : : : : : : : : : : : : : : : :
1410 CACCTTCACGACACTGAGTCTGAGCTCTCTGTGCTTACGAACAGCTGA 1459
    : : : : : : : : : : : : : : : : : : : : : : : :
498 yRLysGlyGlnGlnArgAlaAsn 505
    : : : : : : : : : : : : : : : : : : : : : : : :
1460 TGAATGAGTACAAACAGGCTAAC 1482
    : : : : : : : : : : : : : : : : : : : : : : : :
```

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:z10607

seq_documentation_block:

ID z10607 standard; cDNA; 1993 BP.

```
XX z10607;
XX AC
XX DT
XX 18-NOV-1999 (first entry)
XX cDNA encoding a mechanically sensitive potassium channel protein TREK-1.
XX Mechanically sensitive potassium channel protein; TREK-1;
XX polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
XX nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
XX neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
XX muscular disease; ds.
XX Mus sp.
XX Key Location/Qualifiers
XX CDS 484..1596
XX /*tag= a
XX PN : WO9945108-A2.
XX PD
XX 10-SEP-1999.
XX 23-FEB-1999; 99WO-FR00404.
XX 05-MAR-1998; 98FR-0002725.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX WPI; 1999-551038/46.
XX P-PSDB; Y30648.
XX New mechanically sensitive potassium channel, used to screen for
XX specific modulators, potential therapeutic agents for heart and nervous
XX system disorders
XX Claim 7; Page 23-25; 40pp; French.
XX The present sequence encodes a mechanically sensitive potassium
XX channel protein designated TREK-1. The protein is activated by
XX polyunsaturated fatty acids, particularly arachidonic acid, and by
XX riluzole. The protein is used to screen for specific modulators which
XX are useful for treating or preventing diseases of the heart and nervous
XX systems in humans and animals, e.g. epilepsy, cardiovascular disease
XX (arrhythmia), neurodegeneration (particularly where associated with
XX ischemia or anoxia), abnormalities of hormone secretion and muscular
XX disease. The protein itself may be used to treat these diseases.
XX Antibodies specific for the protein are used to detect it in tissues,
XX also as therapeutic inhibitors or activators.
XX Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 other;
```

alignment_scores:

Quality:	298.50	Length:	316
Ratio:	1.588	Gaps:	13
Percent Similarity:	59.494	Percent Identity:	28.481

alignment_block:

US-08-816-011c-2 x z10607

Align seg 1/1 to: z10607 from: 1 to: 1993

```
9 LeuLeullePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
: : : : : : : : : : : : : : : : : : : : : : : :
631 ATTTTCCTGGTGGTCTCTCTACCTGATCATCGGAGCGCGGTGTCAA 680
: : : : : : : : : : : : : : : : : : : : : : : :
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
: : : : : : : : : : : : : : : : : : : : : : : :
681 GGCATTGGAGCAGCCCTCAGGAG.....ATTCCCGAGAGACCA 718
: : : : : : : : : : : : : : : : : : : : : : : :
```

```
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluLeuGlyAspLysAsn 58
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
719 CCATTGTGATCCAGACGACCTTCATAGCCAGCATGCTGCGTCAAC 768
   XX
59 ThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAspLys 75
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
769 TCCACCGAGCTGGAGAACTCATCAGCAATAATAGTGGCAGCAATAAGCC 818
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
75 sProValThrLeuProProThrTyrAspAspThrProTyrThrTrpThr 92
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
819 AGGGATTATCCCTTAGGAACAGCTCCCAATCAAGTTAGTCACTGGGACC 868
   XX
92 heTyrHisAlaPhePheAlaPheThrValCysSerThrValGlyTyr 108
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
869 TCGGAAGCTCTTCTCTTCTGCTGCTACTGTTATCACAACCATAGGATT 918
   XX
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
919 GGAACATCTCCCAAGCAACTGAAGGTGGAATAATTTCTGCATCATCTA 968
   XX
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly..... 139
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
969 TGCCTTGTGCGGAATCCCTCTTTGGCTTCTACTGCTGGGTGCTG 1018
   XX
140 .....LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1019 ATCAGCTAGGAACATATATTTGGAAGAAGATTTGCCAAGTGAAGACACA 1068
   XX
155 TyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnLe 171
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1069 TTTATTAAAGTGAATGTTAGT.....CAGACGAAGAT 1100
   XX
171 uGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaLeu 188
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1101 TCGTATCATCTCCACCATCATCTCTCTCTTT...GGCTGTCTCTCT 1147
   XX
188 heLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu...Gly 203
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1148 TTGTGGCTCTCCCTCGCGCT.....ATATTCAAGCATATAGAAGC 1188
   XX
204 LeuSerSerIle...SerLeuTyrTyrSerTyrValThrThrThrIle 219
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1189 TGGAGCGCCCTGGAGCGTACTATTTTGGTTATCACTCTGACGACCAT 1238
   XX
219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGlu 236
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1239 TGGATTGGAGACTACGTGGCA..... 1260
   XX
236 heGlyGlyTrpPheValValTyrGlnIlePheVal.....IleValTrp 250
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1261 ..GGTGATCAGACATTGAATATCTGGACTCTTACAAGCCTGTGGTGG 1308
   XX
251 Phe.....IlePheSerLeuGlyTyrLeuValMetIleMetThrPheIle 265
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1309 TTCTGGATCCTCTGTGGCTGGCCCTACTTTCACCTGTCTGACCATGAT 1358
   XX
265 eThrArgGlyLeuGln.....SerLysLysLeuAlaTyrLeuGluGln 280
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1359 TGGGACTGGCTACGGCTGATCTCTAAGAAG.....ACGAAGG 1396
   XX
280 InLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSerGlyVal 296
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1397 AAGAGGTGGAGAGTTTCAGAGCGCATCCCGCTGAGTGGAGCAATGTC 1446
   XX
297 ThrLysAspValGlyTyrLeuArgArgMetLeuAsn...GluLeuTyr 311
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
1447 ACGCCCGAGTTCAAGGAACAGGAGCGGCTGAGCGTGGAGATCTAC 1494
   XX
```

seq_name: /cgn2_2/gcgdata/geneseq/NA1999.DAT:200040

seq_documentation_block:

ID 200040 standard; DNA; 1994 BP.

XX

```
AC 200040;
XX
XX 12-OCT-1999 (first entry)
XX
XX Mouse h-TREK1 polynucleotide.
XX
XX h-TREK1; two pore potassium channel; inflammatory disease;
XX chromosome 1q32; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 484..1719
XX FT /*tag= a
XX FT /product= "h-TREK1"
XX
XX WO9937762-A1.
XX
XX 29-JUL-1999.
XX
XX 02-DEC-1998; 98WO-EF07805.
XX
XX 09-OCT-1998; 98GB-0022135.
XX 27-JAN-1998; 98EP-0300570.
XX
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Chapman CG, Meadows HJ;
XX
XX WPI; 1999-469126/39.
XX P-PSDB; Y28497.
XX
XX New two pore potassium channel used for, e.g. treatment of cancer,
XX pulmonary, cardiovascular and inflammatory diseases
XX
XX Claim 9; Page 25-26; 44pp; English.
XX
XX This sequence is the h-TREK1 polynucleotide from the mouse, encoding the
XX h-TREK1 polypeptide Y28496. h-TREK1 is a two pore potassium channel.
XX The polynucleotide sequence of h-TREK1 can be used to diagnose a disease
XX or susceptibility to a disease related to expression or activity of
XX h-TREK1 polypeptides. The methods of diagnosis may be used in the
XX treatment of diseases including cancer, pulmonary, cardiovascular, and
XX inflammatory diseases, pain, psychiatric disorders including depression
XX and schizophrenia, neurodegenerative diseases including Alzheimer's,
XX stroke, and head trauma and neurological disorders including migraine.
XX
XX Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 other;

alignment_scores:
    Quality: 298.50 Length: 316
    Ratio: 1.588 Gaps: 13
    Percent Similarity: 59.494 Percent Identity: 28.481

alignment_block:
US-08-816-011c-2 x 200040
Align seg 1/1 to: 200040 from: 1 to: 1994
9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaIleTyrTy 25
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
631 ATTTTCCTGGTGGTGGTCTCTACCTGATCGAGCGCGGTGTTCAA 680
   XX
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
681 GGCATTGGAGCAGCCTCAGGAG.....ATTCCCAGAGGACCA 718
   XX
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluLeuGlyAspLysAsn 58
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
719 CCATTGTGATCCAGACGACCATCTCATGCCAGCATGCTGCGTCAAC 768
   XX
59 ThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAspLys 75
```


75 s p r o v a l t h r l e u p r o t h r t y r a s p a s p t h r p r o t y r t h r t r p t h r p 92

DE

```

1077 .....AACCAATCAGGACTGACTC 1090
380 ysLeuAspArgGluLysThrPheGluThrAlaGluAlaTyrHisGlnThr 396
    |||      :|||      :|||      :|||
1099 CTTGTAGGAGG.....ACCTGTCAGTGAAACCACCTGACC 1133
397 ThrAspLeuLeuAlaLysValValAsnAlaLeuAlaThrValLysProPr 413
    :|||      :|||      :|||      :|||
1134 AGCGAG.....AGGGATGCTCTGCCTCC 1156
413 oProAlaGluGlnGluAspAlaAlaLeuTyrGly 424
    |      :|||      :|||      :|||
1157 CTACTGAAGACTGAGAGTATCTATCTGAATGCT 1190

seq_name= /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:z11915
seq_documentation_block:
ID   Z11915 standard; cDNA; 3300 BP.
XX
XX AC
XX AC
XX XX
XX DT
XX DT
XX XX
DE Human potassium channel K-Hnov59 cDNA.
XX
XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's ;
KW cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 50..1285
CDS /*tag= a
FT /*product= "Human K+Hnov59 potassium channel
XX
XX MO9943696-A1.
XX
XX 02-SEP-1999.
XX
XX 22-FEB-1999; 99WO-USO3826.
XX
XX 19-JAN-1999; 99US-O116448.
XX 25-FEB-1998; 98US-0076687.
XX 07-AUG-1998; 98US-0095836.
XX
XX (AXYS-) AXYS PHARM INC.
XX
XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;
XX WPI; 1999-527591/44.
XX P-PSDB; Y34133.
XX
XX New nucleic acids encoding mammalian K+Hnov potassium channel proteins, useful for the diagnosis and treatment of episodic ataxia with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome. Claim 4; Page 102-104; 112pp; English.
XX
XX This sequence represents human potassium channel K+Hnov59 cDNA. K-Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional accessory subunits that act to modulate the channel activity. A 4 transmembrane domain, 2 pore domain potassium channel located on chromosome 19, determined via PCR chromosomal localisation using primers Z11939 and Z11940. K-Hnov cDNAs were isolated by extension of expressed sequence tags (ESTs) related but not identical to known human potassium channels polymorphisms detected as sequence variants between multiple independent clones. Potassium channels have critical roles in cell types and biochemical pathways. Defective potassium channel known to cause four human diseases: episodic ataxia with myoclonic cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical components of virtually all

```

CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+nov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+nov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+nov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.
 xx

SQ Sequence 3300 BP; 997 A; 629 C; 680 G; 994 T; 0 other;

alignment_scores:

Quality: 292.50 Length: 428
 Ratio: 1.306 Gaps: 18
 Percent Similarity: 52.336 Percent Identity: 25.234

alignment_block:

US-08-816-011c-2 x z11915 ..

Align seg 1/1 to: z11915 from: 1 to: 3300

9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
 197 ATATTCCTGGTGGTTCCTCTCTATCTGATCGGACCCACCGCTGTCAA 246
 25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
 247 AGCATTTGGAGCAGCCTCATGAG.....ATTTCACAGAGGACCA 284
 42 laeGlnIleAlaIleAsnGluTyrLeuGluGluLeuGlyAspLysAsn 58
 285 CCATTCTGTGATCCAGAAAGCAACATTCATCCCAACATTCCTGTGCAAT 334
 59 ThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAsp 75
 335 TCGACGGAGCTGGATGAACATTCACGAAATAGTGGCAGCAATAATGC 384
 75 sProValThrLeuProProThrTyrAspThrProTyrThrTyrThrP 92
 385 AGGATATACCGTTAGGAACACCTCCCAATCAATCAGTCACTGGGATT 434
 92 heTyrHisAlaPhePheAlaPheThrValCysSerThrValGlyTyr 108
 435 TGGGAAGTTCCTTCTTCTTGGTGGCAGCTGTATTACAAACCATAGATT 484
 109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAla 125
 485 GGAACATCTCACCGACGACGACGCGGCAAAATATTCGTATCATCTA 534
 125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly..... 139
 535 TGGCTTACTGGGAATTCCTCTTGGTTCCTTCTTGGTGGAGTTGGAG 584
 140LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
 585 ATCAGCTAGGCACCATATTGGAAAGGAATTCGCCAAGTGGGAAGATAC 634
 155 TyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnLe 171
 635 TTTATTAAAGTGAATGTTAGT.....CAGACCAAGAT 666
 171 uGlyLeuIleThrThrValIleAlaLeuIleProGlyIleAlaLeuP 188
 667 TGCATCATCTCAACATCATATTTATATATT...GGCTGTGTACTCT 713
 188 heLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu...Gly 203
 714 TTGTGGCTCTGCCTGGGATC.....ATATTCAACACATAGAGGC 754
 204 LeuSerSerIle...SerLeuTyrTyrSerTyrValThrThrThrTl 219

755 TGGAGTGCCTGGACGCCATTTATTTTGGTTATCACTTAACAATAT 804
 219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
 805 TGGATTGGTACTAGTTGCA..... 826
 236 heGlyGlyTrpPheValValTyrGlnIlePheVal.....IleValTrp 250
 827 ..GGTGGATCCGATATTTGAATATCTGCACTTCTATAAGCCTGTCGTGG 874
 251 Phe.....IlePheSerLeuGlyTyrLeuValMetIleMetThrPheIl 265
 875 TTCTGGATCCTTGTAGGGCTTGTCTTACTTTGTCTGCTGTGAGCATGAT 924
 265 eThrArgGlyLeuGln.....SerLysLysLeuAlaTyrLeuGluGln 280
 925 TGGAGATTGGCTCCGAGTATCTATAAAG.....ACAAAG 962
 280 lnLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSerGlyVal 296
 963 AAGAGCTGGGAGAGTTTCAGAGCACACGCTGCTGAGTGGACAGCAACGTC 1012
 297 ThrLysAspValGlyTyrLeuArgArgMetLeuAsnGluLeuTyrIleLe 313
 1013 ACAGCCGAATTCAAAGAAACAGGAGGCGACTGAGT..... 1048
 313 uLysValLysProValTyrThrAspValAspIleAlaTyrThrLeuProA 330
 1049GTGAGATTATGACAACTGCTCCAGC 1073
 330 rGSerAsnSerCysProAspLeuSerMetTyrArgValGluProAlaPro 346
 1074 GGGCCACCTCCATC..... 1087
 347 IleProSerArgLysArgAlaPheSerValCysAlaAspMetValGlyAl 363
 1088AAGCGGAAGCTCTCG.....GCAGAACTGGCTGGA.. 1117
 363 aGlnArgGluAlaGlyMetValHisAlaAsnSerAspThrAspLeuThrL 380
 1118AACCAATCAGGAGCTGACTC 1139
 380 ysLeuAspArgGluLysThrPheGluThrAlaGluAlaTyrHisGlnThr 396
 1140 CTTGTAGGAGG.....ACCTGTGCTGAGTGAACCTGACC 1174
 397 ThrAspLeuLeuAlaLysValValAsnAlaLeuAlaThrValLysProPr 413
 1175 AGCGAG.....AGGATGCTCTTGCCTCC 1197
 413 oProAlaGluGlnGluAspAlaAlaLeuTyrGly 424
 1198 CTTACTGAAGACTGAGAGTATCTATCTGAATGCT 1231

seq_name: /cgn2_2/gcdata/geneseq/geneseq/NA2000.DAT:A27105

seq_documentation_block:

ID A27105 standard; CDNA; 1182 BP.

XX A27105;

XX 04-AUG-2000 (first entry)

XX Human h-TRAAK cDNA sequence #1.

XX Human; h-TRAAK; potassium channel polypeptide;

KW 2P domain potassium channel; neurodegenerative disease; stroke;

KW psychiatric disorder; neurological disorder; Gene therapy; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FH Location/Qualifiers

```

FT CDS 1..1182
FT FT /*tag= a
XX /product= h-TRAAK protein #1
XX WO200026253-A1.
XX PD 11-MAY-2000.
XX XX
XX PF 03-NOV-1999; 99WO-GB03634.
XX XX
XX PR 03-NOV-1998; 98GB-0024048.
XX PR 07-OCT-1999; 99GB-0023668.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX XX
XX PI Chapman CG, Duckworth DM;
XX PI
XX DR WPI; 2000-365583/31.
XX DR P-PSDB; Y94425.
XX
XX Novel isolated h-TRAAK polypeptides belonging to the potassium channel
XX family of polypeptides, useful for the diagnosis and treatment of
XX h-TRAAK related disorders, e.g. depression and schizophrenia -
XX
XX PS Claim 5; Page 21; 35pp; English.
XX
XX CC Functional genomics was used to identify h-TRAAK polypeptides and
XX h-TRAAK polynucleotides from human tissue samples. h-TRAAK
XX polypeptides have homology to the 2p domain potassium channel family of
XX polypeptides. The h-TRAAK polypeptides and polynucleotides may
XX be used in diagnostic assays for conditions related to h-TRAAK
XX imbalance and for identifying agonists and antagonists of h-TRAAK
XX polypeptides. The h-TRAAK polypeptides and polynucleotides may also
XX be useful for treatment and prevention (e.g. as vaccines) of certain
XX diseases, such as pain, psychiatric disorders including depression and
XX schizophrenia, neurodegenerative disease including Alzheimer's, stroke
XX and head trauma and neurological disorders including migraine and
XX epilepsy. The present sequence is human h-TRAAK-1 cDNA sequence #1.
XX
XX SQ Sequence 1182 BP; 180 A; 408 C; 377 G; 217 T; 0 other;

alignment_scores:
    Quality: 286.00 Length: 319
    Ratio: 1.634 Gaps: 11
    Percent Similarity: 54.859 Percent Identity: 27.900

alignment_block:
US-08-816-011c-2 x A27105 ..
Align seg 1/1 to: A27105 from: 1 to: 1182
7 ileLeuLeuLeuLeuPheTyriLeSerTyriLeuMetPheGlyAlaAlaI 23
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
19 CTGGCCCTGTGGCGGTGCTTCTTACTTGTGTGTGTGTGTGTGTGTGTGT 68
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
23 eTyTyTyHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnA 40
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
69 GTTCCGGGCGCTGGAGCAGCCCCACGAG.....C 97
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
40 rgLysAlaGlnIleAlaIleAsnGluTyriLeuLeuGluGluLeuGlyAsp 56
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
98 AGCAGGCCAGAGGAGGTGGGGGAGTCCGAGAGAAGTTCTCTGAGGGGCC 147
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
57 LysAsnThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrcy 73
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
148 CATCCGTGTGTGACCGACGAGGAGCTGGCTCTCATCAGGAGGTGGC 197
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
73 sAsp.....LysProValThrLeuProProThrTyra 84
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
198 TGATGCCCTGGAGGGGTGGGACCCAGAAACC....AACTCGACCAAGCA 244
   ::::: ||||| ::::: ::::: ||||| ::::: ||||| :::::
84 sAspThrProTyThrTrpThrPheTyrHisAlaPhePheAlaPhe 100

```

```

:::||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
245 ACAGCAGCCACTCAGCCCTGGACCTGGCGACGCCCTTCTTTTCTCAGGG 294
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
101 ThrValCysSerThrValGlyTyriGlyAsnIleSerProThrThrPheAl 117
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
295 ACCATCATCACACATCGGCTATGGCAATGTGGCCCTGGCCGACAGATGC 344
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
117 aglyArgMetIleMetIleAlaTyriSerValIleGlyIleProValAsnG 134
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
345 CGGCGGCTCTTCTGCATCTTTTATGCGCTGTGGGATTCCGCTGTTTG 394
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
134 lyIleLeuPheAlaGlyLeuGlyGluTyriPheGlyArgThr..... 147
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
395 GGATCCTACTGGCAGGGGTGGGACCGCTGGCTCTCTCCTCGGCCAT 444
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
148 .....PheGluAlaIleTyriArgArgTyriLysLysTyriLysMe 160
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
445 GGCATCGGTACATTGAAGCATCTTTTGAAGTGG..... 480
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
160 tSerThrAspMetHisTyriValProGlnLeuGlyLeuIleThrThrV 177
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
481 .....CAGGTGCCACCGGAGCTAGTAAGAGTGTGTGG 514
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
177 alValIleAlaLeuIleProGlyIleAlaLeuPheLeuValLeuProCys 193
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
515 CGATGCTTTCTGCTGATCGGCTGCCTGCTTTTGTCTCCTCACGCCACG 564
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
194 ValGlyValHisLeuLeuArgGluLeuGlyLeuSerSerIleSerLeuTy 210
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
565 TTC...GTGTTCTCTATATGGAGGACTGGAGCAAGCTGGAGGCCATCTA 611
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
210 rTySerTyriValThrThrThrIleGlyPheGlyAspTyriValProT 227
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
612 CTTTGTGATAGTACGCTTACCACCGTGGGCTTTGGGACTATGTGGCC. 660
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
227 hrPheGlyAlaAsnGlnProLysGluPheGlyGlyTyriPheValValTy 243
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
661 .....GGCGGGAGCCCGGAGGAGC.....TCCCGCGCCTAT 693
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
244 GlnIlePheValIleValTrpPheIlePheSerLeuGlyTyriLeuValMe 260
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
594 CAGCGGCTGGTGTGTGTGATCTCTGCGCTGCTTACTTCTTCTGCTC 743
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
260 tileMetThrPheIleThrArgGlyLeuGln.....S 271
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
744 AGTCTCACCCACCATCGGAACTGGCTGGAGTAGTGTCCGCGCGCACTC 793
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
271 erLysLysLeuAlaTyriLeuGluGlnLeuSerSerAsnLeuLysAla 287
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
794 GGCAGAGATGGCGGCTCAGGCTCAGGCTGCCAGC..... 831
   ||::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
288 ThrGlnAsnArgIleTrpSerGly.....ValThrLysAs 299
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
832 .....TGGACTGGCACAGTACACGCGCGGTGACCCACGCG 866
   ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
299 pValGly 301
   ::::: ||||| ::::: ||||| ::::: ||||| ::::: ||||| :::::
867 AGCCGGG 873

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:A27106
seq_documentation_block:
ID A27106 standard; cDNA: 1218 BP.
XX
XX AC A27106;
XX XX
XX DT 04-AUG-2000 (first entry)
XX DE
XX XX
XX XX
XX KW Human; h-TRAAK; potassium channel polypeptide;
XX KW 2p domain potassium channel; neurodegenerative disease; stroke;
XX KW psychiatric disorder; neurological disorder; Gene therapy; ss.

```



```
748 ..... 748
293 TpsrGlyValThrLysAspValGlyTyrLeuArgArgMetLeuAsnG1 309
749 .....AA 750
309 uleuTyrIleLeuLysValLys.ProValTyrThrAspValAspIleAla 325
751 CCTCGTGGTGTCTGCTGCTTATGACCA..... 776
326 TyrThrLeuProArgSerAsnSerCysProAspLeuSerMetTyrArgVa 342
777 ...TGAACCGCGAGGACGAGACCGCG..... 800
342 lGluProAlaProIleProSerArgLysArgAlaPheSerValCysAlaA 359
801 .....ACGCGGAGCACCAGCGC.....TGCTCAC 825
359 spMetValGlyAlaGlnArgGluAlaGlyMetValHisAlaAsnSerAsp 375
826 GCGCAACGGCAGCGGGCGGCGGAGGGGTGGCAGCG..... 866
376 ThrAspLeuThrLysLeuAspArgGluLysThrPheGluThrAlaGluAl 392
867 .....CGCACACTACGGACA..... 881
392 aTyrHisGlnThrThrAspLeuLeuAlaLysValValAsnAlaLeuAla 409
881 ..... 881
409 hrValLysProProAlaGluGlnGluAspAlaLeuTyrGlyGly 425
882 .....CCGCTCATCCAGCGGCGGAGCGGCGGCGGCT..... 917
426 TyrHisGlyPheSerAspSerGlnIleLeuAlaSerGluTrpSerPheSe 442
917 ..... 917
442 rThrValAsnGluPheThrSerProArgArg.....ProA 454
918 .....TCGCAACGCTCTACGGGAGGTGCTGCACCTTCAGTCCAT 957
454 rGlaArgAlaCysSer.....AspPheAsnLeuGluAla 465
958 GTGCTGCTGCTGTGTGAAGAGCGCGAGAGCTGCAGTACTCCATCC 1007
466 Pro.....ArgTrpGlnSerGluArgProLeuArgSerSerHisAs 479
1008 CCATGATCATCCCGGGGACCTCTCCACGTCGACACGTCGCG..... 1049
479 nGluTrpThrTrpSerGlyAspAsnGlnGlnIleGlnGluAlaPheAsnG 496
1050 .....TGGAGC..... 1055
496 lnArgTyrLysGlyGlnGlnArgAlaAsnGlyAlaAlaAsnSerThrMet 512
1056 .....AGAGCCACTCGTCGCGGGAGGGCGGCGCTACAGCG... 1094
513 ValHisLeuGluProAspAlaLeuGluGlnLeuArgAsnAsnHisAr 529
1095 .....ACAGCGCCTCGGACGC 1111
529 gValProValAlaSerArgSerPro.....CysArgMetV 542
1112 TGCTGTGAGCGGGCGGCACCTCCGCATCAGTCCGTGTCACGGG 1161
542 alCysAspValCysPheProSerArgArgSerThrProArgArgIleTrp 558
1162 TCTGCACAGCCTGTCCACCTTCGCGGCGCTCATGAAGCGCA..... 1202
559 SerAlaSerCysProTrpSerArgTyrProArgValSer.SerArgArgL 575
::: 111 ::: 111 ::: 111
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1203 GGAGCTCCGTGTGACTGCCCGGAGGACACCTGGGAGACCTGGGGCGCGGG 1252

575 ysProAspProArgTrpThrThrSerThrArgSerArgArgProPro 591
::: 111 ::: 111
1253 CGGGGAGACCCCTGCTGG.....GAGCCAGGAGACTGCC 1287

592 ValAsnProIleCysAlaThrAspAlaValArgHisArgProSer 606
::: 111 ::: 111
1288 CTGCTGCTCTGCGCAGTGGGACCCGACACAT...CCCTCA 1329

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1997.DAT:T64960

seq_documentation_block:
ID T64960 standard; cDNA; 1894 BP.
XX
AC T64960;
XX
DT 18-MAR-1998 (first entry)
XX
DE TWIK-1 potassium channel cDNA.
XX
KW TWIK-1 potassium channel; screening; diagnosis; transgenic animal;
KW Tandem Of P domains in a Weak Inward rectifying K+; antibody; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 183..1193
FT /tag= a
FT /product= TWIK-1_potassium_channel_protein
XX
PN FR2744730-Al.
XX
PD 14-AUG-1997.
XX
PF 08-FEB-1996; 96FR-0001565.
XX
PR 08-FEB-1996; 96FR-0001565.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Barhanin J, Duprat F, Fink M, Guillemare E, Lazdunski M;
XX Lesage F, Romey G;
XX WPI; 1997-427773/40.
XX P-PSDB; W23397.
XX
XX Nucleic acid encoding new potassium channel designated TWIK-1 -
XX useful for treating channel deficiency diseases, screening for
XX active agents and for diagnosis
XX
XX Claim 3; Figure 1b; 37pp; French.
XX
XX The present cDNA sequence encodes a protein comprising a potassium
XX channel with the properties of a TWIK (Tandem of P domains in
XX a Weak Inward rectifying K+)-1 channel. This is the first member of a new
XX family of channels consisting of 4 transmembrane segments and two P
XX domains, and being only weakly rectifying. The cDNA, vectors, the cells
XX expressing TWIK-1 type channels and the protein are used to compensate
XX for deficiency of potassium channels in various tissues. Compounds
XX for modulating activity of TWIK-1 type channels may also be useful
XX therapeutically, e.g. for control of epilepsy, arrhythmia, vascular
XX disease, neurodegeneration (particularly of ischaemic or anoxic origin),
XX endocrine or muscular disorders. The cDNA and the vectors can also be
XX used to create transgenic animals (especially knock-out animals) for use
XX as models of TWIK-1 related diseases. Analysis of the sequence of the
XX TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies
XX can be used to detect TWIK-1 channels and for inhibiting or activating
XX the channels in vivo.
XX
XX Sequence 1894 BP; 461 A; 435 C; 512 G; 486 T; 0 other;

alignment_scores:

Quality: 239.00 Length: 263
Ratio: 1.583 Gaps: 8
Percent Similarity: 57.414 Percent Identity: 28.137

alignment_block:

US-08-816-011C-2 x T64960 ..

Align seg 1/1 to: T64960 from: 1 to: 1894

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9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
|||.....|.....|.....|.....|.....|.....|.....|.....|
258 CTGGTGGCTGGCTACTCTCTACTGTGCTTCGGCGCAGTGGCTTCTC 307
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
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308 CTCGGTGGAGCTGCCCTATGAGGACCTCTCTGGCCAGGAGCTGGCAGAG 356
42 laGlnIleAlaIleAsnGluTyrLeuLeuGluGluLeuGlyAspLysAsn 58
|||.....|.....|.....|.....|.....|.....|.....|.....|
357 .....CTGAAGCGCGCTCTCTGGAGGAGCAGCAGTGCCTGTCT 395
59 ThrThrThrGlnAspGluIleGluGlnArgIleSerAspTyrCysAspLy 75
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396 GAGCAGCAGCTGGGAGCAGTCTCTGGCGCGGTCTGGAGGCCAGCACTA 445
75 sProValThrLeuProThrThrTyrAspThrProThrThrThrP 92
|||.....|.....|.....|.....|.....|.....|.....|.....|
446 CGGCTGTCTGGTCTCAGCAGCGCTCGGGCAAC...TGGACTGGGACT 492
92 heTyrHisAlaPhePheAlaPheThrValCysSerThrValGlyTyr 108
|||.....|.....|.....|.....|.....|.....|.....|.....|
493 TCACCTCGCGCTCTCTCTGCCAGCAGCGTCTCTCCACACAGGTTAT 542
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
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543 GCCACACCGTCCCTCTGTCAGATGGAGGTAAAGCGCTTCTGCATCACTA 592
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGlyG 142
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593 CTCCTGTCATTGGCATTCCTTCACC...CTCCTGTTC..... 626
142 LuTyrPheGlyArgThrPheGluAlaIleTyrArgTyrLysLysTyr 158
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627 .....CTGACGCGCTGTGTCTCCAGCGCATCACCGTGCAC 659
159 LysMetSerThrAspMetHisTyrValProProGlnLeuGlyLeu..... 173
660 GTCACCGCGCAGCGCGTCTCTACTTCCACATCCGCTGGGCTTCTCCAA 709
174 ....IleThrThrValIleAlaLeuIleProGly.....IleA 186
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710 GCAGGTGGTGGCCATCGTCCATCGCGTCTCTGGTGTCTACTGTGT 759
186 laLeuPheLeuValLeuProCysValGlyValHisLeuLeuArgGluLeu 202
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760 CCGTCTCTCTTCTTATCCGCGCGCTCTCTCTCAGTCTGGAGGATGAC 809
203 GlyLeuSerSerIleSerLeuTyrTyrSerTyrValThrThrThrI 219
|||.....|.....|.....|.....|.....|.....|.....|.....|
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219 eGlyPheGlyAspTyrValProThrPheGlyAlaAsnGlnProLysGluP 236
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860 TGGCTGGGGATATGCTGCTGGGAGGCTACATCAATAA..... 902
236 heGlyGlyTyrPheValValTyrGlnIlePheValIleValTrpPheIle 252
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903 .....TTCAGAGAGCTCTAATGATGGATCAGCTGTACCTGCTA 944
253 PheSerLeu...GlyTyrLeuValMetIleMetThrPhe 264
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seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT.X78383

seq_documentation_block:

ID X78383 standard; cDNA to mRNA; 2180 BP.

XX X78383;

XX 25-AUG-1999 (first entry) }

XX Human hTREK-1 cDNA.

XX hTREK-2; Twik-1 Related K⁺ channel-2; vasotropic; antiinflammatory;
analgesic; treatment; gene therapy; inhibitor; detection; diagnosis;
KW disease susceptibility; cerebral; cardiac; renal; ischemia; brain;
KW inflammation; pain; mimic; neurotransmitter; hormone; chromosome mapping;
KW linkage analysis; mutation; immunogen; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 74..1015

XX FT /*tag= a

XX FT /product= "hTREK-2"

XX EP930364-A1.

XX 21-JUL-1999.

XX 16-JAN-1998; 98EP-0400072.

XX 16-JAN-1998; 98EP-0400072.

XX (SYNO) SYNTHELABO.

XX Partiseti M;

XX WPI; 1999-387707/33.

XX P-PSDB; Y25116.

XX New human polypeptides useful for diagnosing and treating cerebral
and cardiac ischemias

XX Claim 5; Page 15-18; 21pp; English.

XX This invention describes a novel human Twik-1 Related K⁺ channel-2
(hTREK-2) polypeptide (I) and its encoding nucleic acid (II) which has
vasotropic, antiinflammatory and analgesic activity. (II) or agonists of
(I) may be used to stimulate production of (I) in vivo to treat patients
requiring enhanced activity or expression of (I). This use of (II)
represents a gene therapy regime. Antagonists of (I), the complement of
(II) used as an antisense construct or a polypeptide competitor of (I)
may be administered to patients to inhibit activity or expression of (I).
Detection of the presence or amount of (I) in a sample from a patient or
detection of mutations in (I) may be used to diagnose or measure
susceptibility to diseases related to altered expression or activity of
(I). The diseases and conditions resulting from altered activity or
expression of (I) which may be treated as above include cerebral,
cardiac and renal ischemias, brain and cardiac diseases, inflammation
and pain. In addition, (I), (II), and agonists and antagonists of (I)
may be used to mimic or antagonize the effects of endogenous
neurotransmitters and hormones. (II) or its fragments may be used as
hybridization probes to isolate full length and genomic cDNAs encoding
(I) or its homologues from cDNA or genomic libraries. (II) may also be
used for chromosome mapping and linkage analysis to identify the
relationship between genes and diseases which have been mapped to the
same chromosome. In addition (II) may be used to identify mutations
associated with diseases by comparing the sequence of (II) between
affected and unaffected individuals. (I) or its fragments may be used as
immunogens to produce antibodies against (I). Antibodies to (I) may be
used to isolate or identify clones expressing (I) or to purify (I) by
affinity chromatography. These antibodies may also be used to treat the
above diseases as agonists or antagonists of (I).


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XX
SQ Sequence 2180 BP; 374 A; 669 C; 645 G; 492 T; 0 other;

alignment_scores:
  Quality: 210.50      Length: 286
  Ratio: 1.442         Gaps: 9
  Percent Similarity: 51.049 Percent Identity: 24.476

alignment_block:
US-08-816-011c-2 x X78383 ..
Align seg 1/1 to: X78383 from: 1 to: 2180

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26 sIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysAlaG 43
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154 GCTGGAGGGGCCACCAAGCCAGGCTCCAGCCGAG..... 190
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60 ThrThrGlnAspGluLeuGlnArgIleSerAspTyrCysAspLysPr 76
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76 oValThrLeuProThrTyrAsp..... 84
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229 GTGTGTGGTGGCCCGCCGCTGGACGCTTCTGGGAGCGAGTCTGGCGG 278
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84 ..... 84
279 CCGGAGCGGTGGGGTGGTGGTCTTCTTAACGCTTGGGGTCCGCCAAC 328
85 AspThrProTyrThrThrPheTyrHisAlaPhePheAlaPheTh 101
   :||| :||| ||| :|||:|||||:||||| ||
329 GCCTCGGACCCGCTGGGACTTGGCTCTGCTCTCTTCTTCTGCCACG 378
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101 rValCysSerThrValGlyTyrGlyAsnIleSerProThrThrPheAlaG 118
   |||: |||: |||: |||: |||: |||: |||
379 GCTGATCACACCGTGGGCTATGGGTACACACGCGCTGCTGCTGCTG 428
118 lYArgMetIleMetIleAlaTyrSerValIleGlyIleProValAsnGly 134
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429 GCAAGGCTTCTCCATCGCTTTGGCGCTCTGGCGTGGCGGACCATG 478
135 lLeLeuPheAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaI 151
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151 eTyrArgArgTyrLysIleTyrLysMetSerThrAspMetHis..... 165
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529 GCGCCGCTGTGTGCTGATGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 578
166 .....TyrValProGluLeuGlyLeuIleThrThrValValIle 179
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623 .....TGTCTTCTGCTGCTGGCGCTGTGCTGCTGCTGCTGCTGCT 651
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652 CCAC...CTGAGAGGCGCTGGAGCTTCTTGGATGCTTCTTCTTCTGCT 698
213 yrValThrThrThrIleGlyPheGlyAspTyrValProThrPheGly 229
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699 TTATCTCTGTGTACCATCGGCTGGGCGCTGCTGCTGCTGCTGCTGCTG 748
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246 eValIleValTrpPheIlePheSerLeuGlyTyrLeuValMetIleMet. 262
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seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:211914

seq_documentation_block:

ID Z11914 standard; CDNA; 2571 BP.

XX Z11914;

XX 30-NOV-1999 (first entry)

XX Human potassium channel K+Hnov49 cDNA.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
cardiovascular disorder; CNS disorder; renal disorder; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 110..1285

FT /*tag= a

FT /product= "Human K+Hnov49 potassium channel"

FT /note= "No stop codon given in specification"

FT variation 2186

FT /*tag= b

FT /rpt_unit= ATCT

FT /note= "Start site for repeats in 3' untranslated region"

XX W09943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99WO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI: 1999-527591/44.

XX P-PSDB; Y34132.

XX New nucleic acids encoding mammalian K+Hnov potassium channel
proteins, useful for the diagnosis and treatment of episodic ataxia
with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

XX Claim 4; Page 99-101; 112pp; English.

XX This sequence represents human potassium channel K+Hnov49 cDNA.

XX K+Hnov proteins have a high degree of homology to known potassium
channels and may be alpha subunits, which form the functional channel, or
accessory subunits that act to modulate the channel activity. K+Hnov49 is
a 4 transmembrane domain, 2 pore domain potassium channel. The gene's
chromosomal location is 19q41, determined via PCR chromosomal
localisation using primers Z11937 and Z11938. K+Hnov cDNAs

XX were isolated by extension of expressed sequence tags (ESTs) which were
related but not identical to known human potassium channels. Potential
polymorphisms detected as sequence variants between multiple
independent clones. Potassium channels have critical roles in various

CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K-Hnov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K-Hnov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K-Hnov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.
 xx

SO Sequence 2571 BP; 488 A; 744 C; 774 G; 565 T; 0 other;

alignment_scores:
 Quality: 210.50 Length: 286
 Ratio: 1.442 Gaps: 9
 Percent Similarity: 51.049 Percent Identity: 24.476

alignment_block:

US-08-816-011c-2 x Z11914 ..

Align seg 1/1 to: Z11914 from: 1 to: 2571

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26 sileGluHisGlyGluGluTyrlleSerArgAlaGluGlnArgLysAlaG 43
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233 ACGTGTGGGGCGGCGCTTCACGCG.....AGCCG 264
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76 oValThrLeuProThrTyrlleAsp..... 84
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135 IleLeuPheAlaGlyLeuGlyGluTyrllePheGlyArgThrPheGluAlaIl 151
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515 CTGCTGTGACCGCGCTCAGCCGCGCTTCGCTGCTGCTGCTGCTACGT 564
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151 eTyrlleArgTyrlleTyrlleTyrlleMetSerThrAspMetHis..... 165
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565 GCCCCTGTCTGGCTGACATGCGTTCGGGCTGGGACCCCGCGGGCGG 614
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213 yrValThrThrThrIleGlyPheGlyAspTyrlleValProThrPheGly 229
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230 AlaAsnGlnProLysGluPheGlyClyTrpPheValValTyrlleIlePh 246
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246 eValIleValTrpPheIlePheSerLeuGlyTyrlleValMetIleMet. 262
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XX
DT 05-MAY-2000 (first entry)
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DE cDNA encoding KT4, a TWIK family 2PD potassium channel polypeptide.
XX
KW KT4; TWIK family 2PD potassium channel polypeptide; P-domain;
KW expressed sequence tag; EST; A604914; ion channel dysfunction;
KW renal disease; musculoskeletal disease; proliferative disease;
KW renal failure; nephrosis; cirrhosis; dysphagia; gastritis; myotonia;
KW muscular dystrophy; atherosclerosis; cancer; ss.
XX
OS Homo sapiens.
XX
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XX
PN WO200003687-A2.
XX
PD 27-JAN-2000.
XX
PF 20-JUL-1999; 99MO-US16471.
XX
PR 20-JUL-1998; 98US-0093486.
PR 13-AUG-1998; 98US-0096655.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Forsayeth JR, Zhao BB, Chavez RA;
XX
DR WPI; 2000-171196/15.
DR P-PSDB; Y68737.
XX
PT Novel human potassium channel polynucleotides and polypeptides used in
PT the diagnosis, prevention and treatment of diseases including renal
PT failure, cirrhosis, muscular dystrophy and cancers -
XX
XX Claim 14; Fig 1A-C; 53pp; English.
XX

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Date: Mar 17, 2001 7:24 PM
About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

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Query length: 618
Database: Issued_Patents_NA.*
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; Sequence 1, Application US/08332312
; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; TITLE OF INVENTION: Functional Expression of a Drosophila
; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 190..2043
; US-08-332-312-1
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; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; US-08-749-816-1

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; Patent No. 5559026
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; GENERAL INFORMATION:
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; APPLICANT: Price, Laura A.
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; APPLICANT: Pausch, Mark H.
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; TITLE OF INVENTION: Functional Expression of a Drosophila
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; TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast
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; NUMBER OF SEQUENCES: 4
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; CORRESPONDENCE ADDRESS:
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```
; ADDRESSEE: American Cyanamid Company
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; STREET: One Cyanamid Plaza
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; CITY: Wayne
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; STATE: New Jersey
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; COUNTRY: US
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; ZIP: 07470-8426
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1008
; US-08-332-312-3

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  Ratio: 1.271        Gaps: 15
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seq_documentation_block:
; Sequence 2, Application US/08650766D
; Patent No. 6015690
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
; TITLE OF INVENTION: METHOD FOR CLONING THE SAME
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6015690
; CURRENT APPLICATION NUMBER: US/08/650,766D
; CURRENT FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: US 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 1678
; TYPE: DNA
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353 AlaPheSerValCysAlaAspMet.ValGlyAlaGlnArgGluAlaGlyM 369
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609 GCGGCGAGTCCTTCCTGTGATCGAGCTGCCAACACACGGGAGGAGGGCC 658
    |||||:|||||:|||||:|||||:|||||:
369 etValHisAlaAsnSerAspThrAspLeuThrLysLeuAspArgGluLys 385
    |||||:|||||:|||||:|||||:|||||:
659 AGGGTCAACAGGCGGAGGAGGATGAGGAGGAGGAAGAAGAGGAGGAC 708
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386 ThrPheGluThrAlaGluAlaTyrHisGlnThrThrAspLeuLeuAlaLys 402
    :|||:|||||:|||||:|||||:|||||:
709 GTGGCTGAG..... 717

402 sValValAsnAlaLeuAlaThrValLysProProAlaGluGlnGluA 419
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2352 CCGCACAGGAGTCWGGGGGAGCAGCAGACATCTCTCCT..... 2394
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541 etValCysAspValCysPheProSerArgArgSerThrProArgArgIle 557
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2395 ..CCCTGCGCTTGTCTTTCTTCCTCCGCACTGGCGACCTCACCGAGTTG 2442
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
558 TrpSerAla.....SerCysProTrp...SerArgTyrProArgValSe 571
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2443 GCTTCCTCATCCGGAGCTGTCTGTGTCTCAAGGTACGGCACAGTAG 2492
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
571 rSerArg.....LysProAspProArgTyrTrpThrThrSerThrA 586
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2493 AACAGCTCTTCATTATCTCGGAGCGCGCAACCTGCACAGTTCACGC 2542
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586 rg.....SerArgArgProProValAsnProIleCys..... 596
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597 .....AlaThrAspAlaValArgHis..... 603
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2593 CCATCTCTACGGGAGCCACACCGACCTGCAGGAGTTCCTCGGCCAGCTG 2642
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
604 ArgProSerAsnArgMetAlaAlaTyrProAlaAlaAla 616
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2643 CTCACCTCTCACAGG.....TGCGTGGCGCGTGCC 2673
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seq_name: /cqn2_6/ptodata/2/ina/6_COMB.seq:US-08-922-635-3

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seq_documentation_block:
; Sequence 3, Application US/08922635A
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; FISCAL NO. 0053871
; GENERAL INFORMATION:

; APPLICANT: PILETZ, John E.

; APPLICANT: IVANOV, Tina R.

; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES

; TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY

; FILE REFERENCE: Corrected Sequence Listing

; Patent No. 6033871

; CURRENT APPLICATION NUMBER: US/08/922,635A

; CURRENT FILING DATE: 1997-09-03

; EARLIER APPLICATION NUMBER: 08/650,766

; EARLIER FILING DATE: 1996-05-20

; EARLIER APPLICATION NUMBER: 60/012,600

; EARLIER FILING DATE: 1996-03-01

; NUMBER OF SEQ ID NOS: 22

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; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 3

; LENGTH: 3318

; TYPE: DNA

; ORGANISM: Homo sapiens

US-08-922-635-3

alignment_scores:		
Quality:	125.50	Length: 332
Ratio:	0.854	Gaps: 20
Percent Similarity:	44.277	Percent Identity: 25.301

alignment block:

US-08-816-011C-2 x US-08-922-635-3

Align seq 1/1 to: US-08-922-635-3 from: 1 to: 3318

328 LeuProArgSerAsnSerCysProaspLeuSerMet..... 339
 1873 CTTGGCCAGCATCATCTCTCGCTTCCCTTCACTGCTGCTACAGGGCCACC 1922
 340 TyrArg ValGluProAlaPro.....lleProSerArgLysArg 352
 1923 AATCAGGACTTCATCCAGCGCTGAGCACACTGATCGGAGGCCATCGA 1972
 353 AlaPheSerValCysAlaAspMet.ValIGlValAGlnArgGluAlaGlnM 369

APPLICANT: IVANOV, ILLIA K.
TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES

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571 rSerArgArg.....LysProAspProArgTrpThrThrSerThra 586
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2526 AACAGCGCTTCATTATCTCGGAGCGGCCAACCTGCAGAGTCCACGC 2575
    ::| SerArgArgProProValAsnProIleCys..... 596
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2576 GGACCTGGCGCTCATGCTTTGGACCCCGACACATGGCCATGCTGTAGCC 2625
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597 .....AlaThrAspAlaValArgHis..... 603
    ||||| ||| |||
2626 CCATCTCTACGGCAGCCACACAGCGCTCGAGGAGTCTTGCGCCAGCTG 2675
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604 .ArgProSerAsnArgMetAlaAlaThrProProAlaAlaAla 616
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seq_name: /cgn2_6/ptodata/2/lna/6_COMB.seq:US-08-922-635-21

seq_documentation_block:
; Sequence 21, Application US/08922635A
; Patent No. 6033871
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIV
; TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6033871
; CURRENT APPLICATION NUMBER: US/08/922.635A
; CURRENT FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 08/650.766
; EARLIER FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: 60/012.600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 15202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-922-635-21

alignment_scores:
    Quality: 125.50      Length: 332
    Ratio: 0.854        Gaps: 20
    Percent Similarity: 44.277      Percent Identity: 25.301

alignment_block:
US-08-816-011C-2 x US-08-922-635-21

Align seg 1/1 to: US-08-922-635-21 from: 1 to: 15202

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8457 CTGGCCAGATCATCTCTCGCCCTTCACCTGCATTGGCTACACGGCCACC 8506
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340 .TyrArg.ValGluProAlaPro.....IleProSerArgLysArg 352
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8507 .AATCAGAGCTTCATCCAGCGCCTGAGCACACTGATCCGGCAGGCCATCGA 8556
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353 AlaPheSerValCysAlaAspMet.ValGlyAlaGlnArgGluAlaGlyM 369
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8557 GCGGACAGCTGCCTGTGATCGAGCTGCCAACACGCGGAGGAGGGCC 8606
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369 etValHisAlaAsnSerAspThrAspLeuThrLysLeuAspArgGluLys 385
    ||| ::|::| ||| ||| ::|::| ||| |||
8607 AGGCTCAACAGCGCGGAGGAGGATGACGAGGAGGAGGAGGAGGAGGAG 8656
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386 ThrPheGluThrAlaGluAlaTyrHisGlnThrThrAspLeuLeuAla 402
    ||| ::| |||
8657 GTGGCGTGAG..... 8665

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188PheLeuValLeuPro.....CysValGlyValHisLeuLe 199
3677 GATCACGTGTTCTCTGGTGCCTGCCAACACCTGT..... 3709
199 uArgGluLeuGlyLeuSerSerLeuLeuTyrSerTyrValThr. 215
3710CTGGGATGGCATCAGCAGTTCTACGAGAACTACGAGACGC 3752
216ThrThrIleGlyPheGlyAspTyrValProThrPse 228
3753 GGAGGTACTGCACCTCTCCGAGGTGCGCCGCCACCTACTCGAAGAAATAT 3802
229 GlyAlaAsnGlnProLysGluPheGlyGlyTyrPheValVal...TyrGI 244
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3803 AACATCCAGTACCAGAGAACTTCTATGCTGGAGGCCCGCGGGGTGCG 3852
244 nIlePheValIleValTrpPheIlePheSerLeuGlyTyrLeuValMetI 261
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3853 CCGGTTTGTGGCTTCATGGCGGCTCAGGGTGGCTACCTCATCTGCTGC 3903
261 leMetThrPheIleThrArgGlyLeuGlnSerLysLysLeuAlaTyrLeu 277
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3903 TCTTCCTCATCGAGACCAAC.....CTG 3925
278 GluGlnGlnLeuSerSerAsnLeuLysAlaThrGlnAsnArgIleTrpSe 294
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294 rGlyValThrLysAspValGlyTyrLeuArgMetLeuAsnGluLeuT 311
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3965AGCGCGACACTGCACAGAAATAT 3986
311 yrIle...LeuLysValLysProValTyrThrAspValAspIleAla... 325
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3987 ACACCGGATGCCGTGCTTCCT.....GAGGACCAAGATGAGCGGAC 4030
326TyrThrLeuProArgSerAsnSer.Cys.ProAspLeu 337
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338 SerMetTyr.....ArgValGluProAlaProI 347
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4081 TCTGATTATCAAGAGACTCTCCAAGGTGTACGAGACGGGTGCCCTC.. 4128
347 eProSerArgLysArgAlaPheSerValCysAlaAspMetValGlyAlaG 364
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4129 .CCTGGCCGTGGACAGCTCTCCTCGCGGTGCAGAAAG...GGAGTGC 4174
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4175 TTCGGCTGCTGGCTTCAATGGAGCGGGAGACACCGACTTTCAAAAT 4224
381 LeuAspArg.GluLysThrPheGluThrAlaGluAlaTyr.....H 394
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4225 GCTACCGGGGAGAGAGACTCTACTTCTGGGGATGCTTGTTCGGGGGTC 4274
394 isGlnThrThrAspLeuAlaLysValValAsnAlaLeuAlaThrVal 410
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4275 ACAGAATCAGCTGTGATGTCGGAAGAGTGGCGGAGCGGATCGGCTAC... 4321
411 LysProProAlaGluGlnGluAspAlaAlaLeu..... 422
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4510 GAGCACCGCATCCGCCTCATCGGAGAGCCTGCTGTCATCTTCTCGACG 4559
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454 uAlaProArgTrpGlnSerGluArg...ProLeuArgSerSerHisAsnG 480
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4560 ACCCTCCATCGCATCGAGACCOCCTGGCCGCGCTGCTTTGGGACAC 4609
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480 LuTrpThr.....TrpSerGlyAspAsnGlnGlnIleGlnGlu 492
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4610 GTGGCAGGAGCCGAGAGTCTGGCAGGCGCATCATCACTCCCACAG 4659
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493 AlaPheAsnGlnArgTrpLysGlyGlnGlnArgAlaAsnGlyAlaLaas 509
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4660 CATGGAGGAGTGAGGCCCTGTGCACCCGCTGGCCCATCATGTCGACG 4709
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509 nSerThrMetValHisLeuGluProAspAlaLeuGluGlnLeuArgA 526
      :||| ::|||::| | | | | |
4710 GCAGTTCAAGTGCCTGGCGCCGCCAGCCTCAAAGAGCAAGTTCGGC 4759
      :||| ::|||::| | | | | |
526 snAsnHisArgValProValAlaSerArgSerSerProCysArgMetVal 542
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4760 ACGG.....GCTACTCCCTCGCGGGCCAAGG 4784
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543 CysAspValCysPheProSerArgArgSerThrProArgArgIleTrpSe 559
      :||| ::|||::| | | | | |
4785 TGC.....AGAGTAGAGGCGACAGAGGCGCTGGAG 4816
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559 rAlaSerCysPro...TrpSerArgTrpProArgValSerSerArgArgL 575
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4817 GAGTTCAAGCGCTTCGTGGACCTGACCTTCCAGGCGAGCGTCTCGGAAGA 4866
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575 ysProAspProArgTrpThrThrSerThrArgSerArgArgProPro 591
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-762-500-24

seq_documentation_block:
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; METHOD OF MAKING AND USING THE SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
; US-08-762-500-24

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alignment_scores:
  Quality: 124.50      Length: 596
  Ratio: 0.454        Gaps: 34
Percent Similarity: 45.973 Percent Identity: 22.148

alignment_block:
US-08-816-011c-2 x US-08-762-500-24
Align seg 1/1 to: US-08-762-500-24 from: 1 to: 5894

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113 oThrThrPheAlaGlyArgMetIleMetIleAlaTyrSerValIleGlyI 130
3481 CACCCG.....CTGCTGCTCTGCTACGGTGGGCCATCA 3518
130 leProValAsnGlyIleLeuPheAlaGlyLeuGlyGluTyrPheGlyArg 146
3519 TCCTCCCTCATGTACCTGATG.....NACTTCTTCTCTTG 3553
147 ThrPheGluAlaIleTyrArgTyrTyrLysLysTyrLysMetSerThrAs 163
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294 rGlyValThrLysAspValGlyTyrLeuArgArgMetLeuAsnGluLeuT 311
3965 .....AGCGGACACTGACAGAAATAT 3986
311 yrIle...LeuLysValLysProValTyrThrAspValAspIleAla... 325
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338 SerMetTyr.....ArgValGluProAlaProI 347
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364 lnArgGluAlaGlyMetValHisAlaAsnSerAspThrAspLeuThrLys 380
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381 LeuAspArg.GluLysThrPheGluThrAlaGluAlaTyr.....H 394
4225 GCTCACCGGGGAGGAGACCTCACTTCTGGGATGCTTTTTCGGGGTGC 4274
394 isGlnThrThrAspLeuAlaLysValValAsnAlaLeuAlaThrVal 410
4275 ACAGATCAGCTCTGATGTCGGAAGGTGCGGAGCGGATCGGCTAC... 4321
411 LysProProAlaGluGlnGluAspAlaAlaLeu..... 422
4322 .....TGCCCGCAGTTTGTATGCTTGTGGACCATGACAGG 4359
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433 lnIle..... 434
4410 ACATCGGGCTGGTGAGAACACTCTCGGGGCTGCTGCTGGAGCCA 4459
435 LeuAlaSerGlu.TrpSerPheSerThrValAsnGluPheThr..... 448
4460 CATGCCAACAGCTGGTCAGGACCTACAGTGGTGTAAACAGCGGAAGCT 4509
449 ..SerPro.ArgArgProAlaArgAlaCysSerAspPheAsnLeuGI 464
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US-08-447-965A-1

alignment_scores:

Quality: 124.00 Length: 349
Ratio: 0.832 Gaps: 18
Percent Similarity: 42.693 Percent Identity: 25.788

alignment_block:

US-08-816-011c-2 x US-08-447-965A-1/rev ..

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345 aProIleProSerArgLysArgAlaPheSerValCysAlaAsp..... 359
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1278 GCGCGCCGCTCGGCTGGGGT.....CCCGTTGGCCAGATCGGCCAG 1235
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360 .....MetValGlyAlaGlnArgGluAlaGlyMet 369
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1234 TTCTCCGCCACGCGCCAGCTGTCCGCCCGCATCGCGGGCGGAGAN 1185
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1184 GTCGTTGGCGGCTGTGCAGGAACGCAACACAGAGCGGCGAGACCAAGCA 1135
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386 rPheGluThrAlaGluAlaTyrHisGlnThrAspLeuLeuAlaLysV 403
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1134 GTTC....GTGCGCGCATCTCCAGCGGCTCACCGACCTGGCGGCGCGG 1088
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403 alValAsnAlaLeuAlaThrValLysProProAlaGluGlnGluAsp 419
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1087 TGACC.....GCGCGGAGMACATGCC 1065
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420 AlaAlaLeuTyrGlyGlyTyrHisGlyPheSerAspSerGlnIle..LeuA 436
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seq_documentation_block:

; Sequence 17, Application US/08510646B
; Patent No. 6077699

GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique
; APPLICANT: Blanc, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie

TITLE OF INVENTION: Polypeptides Involved In The

TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences

TITLE OF INVENTION: Coding For These Polypeptides And Their Use

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICANT NUMBER: US/08/510,646B

FILING DATE: 03-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/403,852

FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR 93/00923

FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441

FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-01000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2219 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
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 US-08-510-646B-17

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Date: Mar 17, 2001 6:53 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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Database: EST.*
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Database length: 791223438
Search time (sec): 885.420000

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SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 582)
AUTHORS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
P., Lewis,S. and Rubin,G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2286367.
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
Plate: 192 row: C column: 12
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 487)
AUTHORS Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein
, P., Lewis, S. and Rubin, G.M.
TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
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525 rGAsnAsnHisArgValProValAlaSerArgSerSerProCysArgMet 541
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53 GAAACAATCACCGGTGCGGTCGCGTCGCTCAAGAAGTTCTCCATGCCGGATG 102
|||||
542 ValCysAspValCysPheProSerArgSerThrProArgArgIleTr 558
|||||
103 GTCTGCGACGCTCTGTTTCCCTTCAGAAAGCGCCCTCCGAGGATCTG 152
|||||
558 pSerAlaSerCysProTrpSerArgTyrProArgValSerSerArgArgL 575
|||||
153 CAGCGCAAGTTGTCGCTCGGTCTCGGTACCCGAGGCGTGTCTCATCGCAGCA 202
|||||
575 ysProAspProArgTrpThrThrSerThrArgSerArgArgProPro 591
|||||
203 AGCCAGATCCCGCTGGACTACTACAGCACACGCTACGGCGGCTCCA 252
|||||
592 ValAsnProIleCysAlaThrAspAlaValArgHisArgProSerAsnAr 608
|||||
253 GTCAATCCTATTGCGCAACGAGCGGTCGCGCACCGCCCTTCGATCG 302
|||||
608 gMetAlaAlaTrpProAlaAlaAlaAlaGly 618
|||||
303 AATGGCAGCTTGGCAGCGGCGCGCGCGGC 333
|||||

seq_name: gb_est74:BE680493

seq_documentation_block:
LOCUS BE680493 586 bp mRNA EST 11-SEP-2000
DEFINITION df81b01.y1 Xenopus laevis oocyte non normalized xenopus laevis cDNA
clone XENOPUS_SOURCE_ID:xlnnoc002m02 5' similar to TR:095279 095279
TWO PORE DOMAIN K+ CHANNEL. ;, mRNA sequence.
ACCESSION BE680493
VERSION BE680493.1 GI:10064401
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 586)
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
, Martin, J., Wylie, I., Underwood, K., Theising, B., Bowers, Y., Person
, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
Other_ESTs: df81b01.x1
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnnoc002m02
Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers
1..586
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnnoc002m02"

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FEATURES
Source

469 CATCACTATCACCACCATTGGGTTTGGAGACTATGTTGCANGTGTGAATC 518

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230  laAsn 231
      |||
519  CCAAT 523

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seq_name: qb est22:AI605559

seq: documentation block.

LOCUS	AT605359	6
DEFINITION	ma07b04 v1	score

IMAGE: 303895 57
ACTD-SENSITIVE

ACCESSION AI605559

KEYWORDS , EST.

ORGANISM *Mus musculus*

Mammalia; Eutheria

AUTHORS Marra, M., Hillier

, B., Swaller, T.

Waterston, R. and

JOURNAL Unpublished (1991)

Washington University

4444 FOTESC FALL
Tel: 314 286 180

Fax: 314 266 16...
Email: mouseest...

THIS CLONE IS AN
IMAGE CONCEPT

This road is a

correct orientation

MGI:200655

High quality seed

FEATURES

/organ:

/clone=

```
/dev/st
```

/note=

polyimide was prepared

double:

adapters
the Not

(pharmacokinetic parameters)

Soares
Dr. M. L.

BASE COUNT 113 a 21.

alignment_scores:

Ratio: 1.788

Form

alignment_block:

US-08-816-011c-2 x AI605559

Align seg 1/1 to: AI605559 from: 1 to: 677

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5 ArgTrpIleLeuLeuLeuLeuPheTyrIleSerTyrLeuMetPheGlyAl 21
9 CGCAGTTGGCTCTCATCGTGTGCACCTTACCTACCTGCTGGTGGCGC 58
21 aAlaIleTyrTyrHisIleGluHisGlyGluGluLysIleSerArgAlaG 38
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
59 CGCGGTGTTCCAGCACACATGGAGTCGGAGCCGGAGATGATCGAGCGG 108
38 luGlnArgLysAlaGlnIleAlaIleAsn...GluTyrLeuLeuGluGlu 53
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
109 GGCTGGAGCTGGCGCAGCTGGAGCTGGCGCGCGCTCAACACTCAGCGAG 158
54 LeuGlyAspLysAsnThrThrThGlnAspGluIleLeuGlnArgIleSe 70
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
159 GCGCGC.....TACGAGGAGCTGGAGCGGCTC... 185
70 rAspTyrCysAspLysProValThrLeuProProThrTyrAspThrP 87
   :::::|||||:|||||:|||||:|||||:|||||:|||||:
186 .....GTGCTGGCGCTCAAGCG.....CACAGGCGC 213
87 roTyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCys 103
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 CGGTGCAGTGGCGTTCGCCGCGCTCTTACTTCGCCCATCACCCTCATC 263
104 SerThrValGlyTyrGlyAsnIleSerProThrPheAlaGlyArgMe 120
264 ACCACCATCGCTATGTCATGTCGCGCGCCAGCAGCGGAGGCAAGGT 313
120 tIleMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuP 137
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
314 GTTCGATGTTTCACGCGCTGCTGGGCATCCGCTCACATAGTCATGT 363
137 heAlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 TCCAGAGCGCTGGTGAACGCATCAAC.....ACCTTCGTG 398
154 ArgTyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlu 170
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
399 AGGTACCTGCTGCACCGCTGCCAAGAGGGGCTGGGCATCGCGCAGCGCA 448
170 nLeuGlyLeuIleThrThrValValIleAlaLeuIleProGlyIleAlaL 187
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
449 GGTGCCATGCCCAACATGGTGTCTCATCGGTTTCGTGTCATCAGCA 498
187 euPheLeuValLeuProCysValGlyValHisLeuLeuArg.....Glu 201
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
499 CGCTG.....TGCATCGCGCAGCTGCCTTCTCTACTACTACGAG 536
202 LeuGlyLeuSerSerIleSerLeuTyrTyrSerTyrValThrThrTh 218
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
537 CGCTGGACTNTCTCCAGGCGCTATTACTGCTTCAATCACCCTCACCA 586
218 rIleGlyPheGlyAspTyrVal 225
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
587 CATCGGCTTCGCGCATATGTG 608

```

seq_name: gb_est45:AW506290

seq_documentation_block:

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LOCUS      AW506290              671 bp      mRNA      EST      02-MAR-2000
DEFINITION GE1674 Globodera rostochiensis J2 pCDNAII Globodera rostochiensis
            cDNA similar to potassium channel subunit, mRNA sequence.
ACCESSION  AW506290
VERSION    AW506290.1  GI:7144182
KEYWORDS   EST.
SOURCE     Globodera rostochiensis.
            Globodera rostochiensis
ORGANISM   Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

```

Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

REFERENCE 1 (bases 1 to 671)
 AUTHORS Popeijus, H., Blok, V.C., Bakker, E., Cardle, L., Phillips, M.S., Helder, H., Smant, G. and Jones, J.T.

TITLE Analysis of genes expressed in second stage juveniles of the potato cyst nematode Globodera rostochiensis and G. pallida using the expressed sequence tag approach

JOURNAL Unpublished (2000)

COMMENT

Contact: Jones JT

Nematology Department

Scottish Crop Research Institute

Invergowrie, Dundee, DD2 5DA, UK

Tel: 44 1482 562731

Fax: 44 1382 562426

Email: j.jones@sari.ac.uk

POLYA=NO.

FEATURES

source

Location/Qualifiers

1..671

/organism="Globodera rostochiensis"

/db_xref="taxon:31243"

/clone_lib="Globodera rostochiensis J2 pCDNAII"

/dev_stage="Second stage juvenile"

/note="Vector: pCDNAII (Invitrogen); Site_1: EcoRI;

Site_2: NotI; mRNA extracted from preparasitic J2s of

Globodera rostochiensis cloned directionally into pCDNAII

plasmid vector."

BASE COUNT 125 a 172 c 181 g 193 t

ORIGIN

alignment_scores:

Quality: 228.00 Length: 216

Ratio: 1.949 Gaps: 7

Percent Similarity: 54.167 Percent Identity: 28.241

alignment_block:

US-08-816-011c-2 x AW506290

Align seg 1/1 to: AW506290 from: 1 to: 671

```

89 ThrTrpThrPheTyrHisAlaPhePhePheAlaPheThrValCysSerTh 105
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:
19 AGTTGGAGCATGACAACGGCAGTGTCTTCACCTCCACTCTGTTGACCA 68
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
105 rValGlyTyrGlyAsnIleSerProThrPheAlaGlyArgMetIleM 122
   |::|||:|||||:|||||:|||||:|||||:|||||:|||||:
69 CATCGGATACGGTAATTGGTGCAGTACTCCGCCGGCGGAATGTTCT 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 etIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPheAla 138
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GCATTTTCTACGCTCTCTTTGGCGTTCGGCTGATTCATCATCTGCTCG 168
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArgArgTy 155
   |::|||:|||||:|||||:|||||:|||||:|||||:|||||:
169 GACATTTGAAAGTTCTTCTCGACTTGTATTGTTCTGTTGTACACGCA 218
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
155 rLysLysTyrLys..... 159
   |:::|||||
219 CACACGCGCAAACTTCGCTGGGGGAGCAGACTGTTGGCGCGCTGGCG 268
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
160 .....MetSerThrAspMetHisTyr 166
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 GGGAGGAGCGCGCGGAGATCCAAACGGTATTGAGAGCGCATCTGCAC... 315
167 ValProGlnLeuGlyLeuIleThr...ThrValIleAlaLeuIle 182
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
316 .....CAGTTGGGCGCTTTACACATTTTCCATTCGCCGTCACATGAT 356
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 eProGlyIleAlaLeuPheLeuValLeuProCysValGlyValHisLeuL 199
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
357 C.....GCCGCCATTCTCTCGGCTACATGAGCATCGTCCCGCTCTTT 400
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 euArgGluLeuGlyLeuSerSerIle.....SerLeuTyrTyrSerTyr 213

```



```

FEATURES
  source
    High quality sequence stop: 450.
    Location/Qualifiers
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        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="IMAGE:421453"
        /clone_lib="Soares mouse embryo NBMel3.5 14.5"
        /sex="unknown"
        /tissue_type="embryo"
        /dev_stage="13.5-14.5dpc total fetus"
        /lab_host="DH10B"
        /note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTCGGCGCGCGCGGAAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M. Fatima Bonaldo."
BASE COUNT      82 a 160 c 137 g 104 t
ORIGIN
alignment_scores:
  Quality: 193.50      Length: 138
  Ratio: 2.224        Gaps: 3
  Percent Similarity: 63.043      Percent Identity: 30.435
alignment_block:
US-08-816-011c-2 x AL325858
Align seg 1/1 to: AL325858 from: 1 to: 483
90 TrpThrPheTyrHisAlaPhePheAlaPheThrValCysSerThrVa 106
||| ||| :|||:|||||:|||||:|||||:|||||:
37 TGGCGCTTCGCGGCTCTTCTACTTCGCCATCACCCTCATCACCAT 86
106 lGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetI 123
:|||||:|||||:|||||:|||||:|||||:|||||:
87 CGCTATGTCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 136
:|: |||:|||||:|||||:|||||:|||||:|||||:
123 leAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPheAlaGly 139
:|: |||:|||||:|||||:|||||:|||||:|||||:
137 TGTCTACGGCTGTGGGCTATCCGCTCACACTAGTGTCCAGAGC 186
140 LeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArgTyrLy 156
||||||| :|||:
187 CTGGGTGAAGCATCAAC.....ACCTTCGTGAGGTACCT 221
156 sLysTyrLysMetSerThrAspMetHisTyrValProGlnLeuGlyL 173
:|||||: |||: |||:
222 GCTGCACCGTGCACAGAGGGCGCTGGCGCATGCGCGCATGCGGTGCCA 271
173 eutIleThrValValIleAlaLeuIleProGlyIleAlaLeuPheLeu 189
:|: |||:|||||:|||||:|||||:|||||:
272 TGGCCACATGGTGTCTATCGGTTTGTGTCTGTCATCAGCAGCGTGG... 318
190 ValLeuProCysValGlyValHisLeuLeuArg.....GluLeuGlyLe 204
||||||| :|||:
319 .....TGCATCGCGCAGCTGCTCTCTCTACTACGAGCGCTGGAC 359
204 uSerSerIleSerLeuTyrTyrSerTyrValThrThrThrIleGlyP 221
:|: |||:|||||:|||||:|||||:|||||:
360 TTTCTTCCAGCGCTATTACTACTGCTTCTTCTTCTTCTTCTTCTTCT 409
221 heGlyAspTyrVal 225
|||||||
410 TCGCGCACTATG 423
seq_name: gb_est37:AV612885
seq_documentation_block: 607 bp mRNA EST 30-AUG-2000
LOCUS AV612885 Bos taurus lung fetus Bos taurus cDNA clone ELLU048D11 5',
DEFINITION AV612885 Bos taurus lung fetus Bos taurus cDNA clone ELLU048D11 5',
mRNA sequence.
ACCESSION AV612885
VERSION AV612885.1 GI:9748555
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 607)
AUTHORS Sugimoto, Y., Hirotsume, S., Takasuga, A., Itoh, R., Jitohzono, A. and
Suzuki, H.
TITLE bovine cDNA sequencing
JOURNAL unpublished (2000)
CONTACT Yoshikazu Sugimoto
COMMENT Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-23-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
  source
    Location/Qualifiers
      1..607
        /organism="Bos taurus"
        /db_xref="taxon:9913"
        /clone="ELLU048D11"
        /clone_lib="Bos taurus lung fetus"
        /tissue_type="lung"
        /dev_stage="fetus"
        /lab_host="DH10B"
        /note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT      118 a 184 c 148 g 157 t
ORIGIN
alignment_scores:
  Quality: 186.50      Length: 184
  Ratio: 1.759        Gaps: 6
  Percent Similarity: 57.609      Percent Identity: 29.891
alignment_block:
US-08-816-011c-2 x AV612885
Align seg 1/1 to: AV612885 from: 1 to: 607
88 TyrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCysSe 104
:|||||: |||: |||:|||||:|||||:|||||:
24 TGAACCTGGGACTTCACCTCGCGCTCTTCTGCGCAGCACCGTGTCTC 73
104 rThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetI 121
|||||:|||||:|||||:|||||:|||||:|||||:
74 CACACAGGTTCAGGCACACACCGTGTCTGCGCAGCGGGGCAAGGCCT 123
121 leMetIleAlaTyrSerValIleGlyIleProValAsnGlyIleLeuPhe 137
:|: |||:|||||:|||||:|||||:|||||:
124 TCTGCATCATCTATTCGTCATCGGCATACCTTTCACC...CTTCGTTC 170
138 AlaGlyLeuGlyGluTyrPheGlyArgThrPheGluAlaIleTyrArg 154
:|: |||:|||||:|||||:|||||:
171 .....CTGACGGCAGTGGTCCAGCG 190
154 gTyrLysLysTyrLysMetSerThrAspMetHisTyrValProGlnL 171
:|: |||:
191 TGTACCATCATGTACACCGCAGCGAGTCTCTACTTCCACGTCCGCT 240
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DEFINITION UI-M-CG0p-bdb-f-11-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
ACCESSION BE981393
VERSION BE981393.1 GI:10650455
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 593)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-NO.

FEATURES source
1..593
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bdb-f-11-0-UI"
/lab_host="NIH_BMAP_Ret4_S2"
/note="vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"
BASE COUNT 129 a 179 c 165 g 119 t 1 others
ORIGIN

alignment_scores:
Quality: 183.00 Length: 193
Ratio: 1.794 Gaps: 6
Percent Similarity: 52.850 Percent Identity: 26.943
alignment_block:
US-08-816-011C-2 x BE981393/rev ..
Align seg 1/1 to reverse of: BE981393 from: 1 to: 593
7 TleLeuLeuLeuPheTyrlleSerTyrLeuMetPheGlyAlaAla1 23
::: ||||| :::: |||||::: ||||| :::
536 CTGGCTCTGCTGGCACTGCTGCTGCTTACTTGGTATCTGGGGCTCTAGT 487
23 eTyrTyrlleGlu..... 28
::::: |||||
486 GTTCCAGGCTCTGGAGCAGCCTACAGCAGCAGGCTCAGAGAAATGG 437
29 ..HisGlyGluGluGlyIleSerArgAlaGluGlnArgLysAlaGlnIle 44
|||||:::|||||::: ||| :::
436 ATCATGGCCGAGACCACTAGTTCTCTGAGGAGCCATCCCTGTGTGACCCAGAG 387

45 AlaIleAsnGluTyr.....LeuLeuGluGluLeuGlyAspLysAs 58
:::|||||::: |||||::: |||||
386 AGCCTGGAGGATTTCATCAAGCTCTGGTGAAGCCCTGGAGGGGC... 339
58 nThrThrThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAspL 75
338GCAA 335
75 yProValThrLeuProProThrTyrAspThrProTyrThrTyrThr 91
::: ||| :::: |||||::: |||||
334 ACCCAACACCGAGCTGGACCAATAGCAGCAACCACTCATCAGCTTGAAC 285
92 PheTyrHisAlaphePheAlapheThrValCysSerThrValGlyTy 108
::: |||||::: |||||::: |||||
284 CTGGGCGAGCGCTCTCTTCTCGGGGACCATCATCATTACCATCGGCTA 235
108 rGlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAla 125
|||||::: ||| |||||::: |||
234 TGGCATATAGTCTTACACACAGATCGCGGGCTCTCTTTGTATCTTCT 185
125 yrSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGly 141
||:|||||::: |||||::: |||||
184 ATGCACTGTGGGATCCCACTCTTCGGGATGCTGCTGGCGGAGTCGGG 135
142 GluTyrPheGlyArgThr.....PheGluAlaIle 151
::: ||| :::: |||||::: |||||
134 GACCGCTGGGCTCTCTCTCGCGCGGCGGATCGGCACATCGAAGCAAT 85
151 eTyrArgTyrLysLysTyrLysMetSerThrAspMetHisTyrValp 168
||:|||||::: |||||
84 CTCTTGAAGTGG.....CATGTGC 65

168 rProGlnLeuGlyLeuIleThrVal 177
|||||::: |||||
64 CACCG.....GGCTGTGAGAGTCTG 42

seq_name: gb_est7:AA464375

seq_documentation_block:
LOCUS AA464375 401 bp mRNA EST 10-JUN-1997
DEFINITION zx81d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:810165 5' similar to TR:G1086491 G1086491 TWIK-1.; mRNA
sequence.
ACCESSION AA464375
VERSION AA464375.1 GI:2189259
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 401)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,
T., Waterston,R. and Willson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

TITLE
JOURNAL
COMMENT This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 315.
Location/Qualifiers
1..401
/organism="Homo sapiens"
/db_xref="GDB:6040286"
/db_xref="taxon:9606"
/clone="IMAGE:810165"

FEATURES source
1..401
/organism="Homo sapiens"
/db_xref="GDB:6040286"
/db_xref="taxon:9606"
/clone="IMAGE:810165"

```

ORGANISM      Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.

REFERENCE
AUTHORS      Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.
              Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
              J.W., Bonaldo,M.F. and Soares,M.B.
              The NIHES Xenopus Maternal EST Project
              Unpublished (2000)
COMMENT      Contact: Perry J. Blackshear
              Office of Clinical Research and Laboratory of Signal Transduction
              National Institute of Environmental Health Sciences
              A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
              USA
              Tel: 919 541-4899
              Fax: 919 541-4571
              Email: black009@niehs.nih.gov
              Clone is available through Research Genetics, Inc., 2130 Memorial
              Parkway, Huntsville, AL 35901
              phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
              cdna@resgen.com
              DNA Sequencing and analyses performed by National Institutes of
              Health Intramural Sequencing Center (NISC).
              PCR Primers
              FORWARD: TGTTAAACGACGGCCAGT
              BACKWARD: CAGGAACAGCTCATGCC
              Plate: 0136 row: H column: 06
              Seq primer: T7 primer.
              Location/Qualifiers
                source          1..632
                  /organism="Xenopus laevis"
                  /db_xref="taxon:8355"
                  /clone="PBX0136H06"
                  /clone_lib="Blackshear/Soares normalized Xenopus egg
                  library"
                  /sex="female"
                  /tissue_type="unfertilized egg"
                  /cell_type="unfertilized egg"
                  /dev_stage="unfertilized egg"
                  /lab_host="DH10B"
                  /notes="Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI;
                  PolyA-selected mRNA was prepared from unfertilized Xenopus
                  laevis eggs. The library was constructed in the vector
                  pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
                  Soares, M.B. 'Normalization and subtraction: two
                  approaches to facilitate gene discovery', Genome Research
                  6:791-806, 1996. The first strand synthesis used a
                  NotI-dT18 primer; double stranded cDNAs were ligated to
                  EcoRI adapters, digested with NotI, and directionally
                  cloned into the NotI and EcoRI-digested pT73-Pac vector.
                  The library contained approximately 7.2 X 10^5
                  recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT   146 a   176 c   173 g   137 t
ORIGIN

alignment_scores:
  Quality: 175.00      Length: 144
  Ratio: 1.923        Gaps: 3
  Percent Similarity: 63.194      Percent Identity: 32.639

alignment_block:
US-08-816-011C-2 x AW644141 ..

Align seg 1/1 to: AW644141 from: 1 to: 632

4 AsnArgTTPileLeuLeuLeuLeuPheTyrIleSerTyrLeuMetPheG1 20
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
225 GACCGGGGACCCATCCTGACATCTGCGGTCACTCTTCACTGTCCATGG 274
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
20 yAlaAlaIleTyrTyrHisLeuHisGlyGluGluLysIleSerArgA 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```
/clone_lib="Soares ovary tumor NBH07"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTCAAGTGGGCGGCCGGTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      111 a      83 c      86 g      121 t
ORIGIN

alignment_scores:
    Quality: 175.50          Length: 141
    Ratio:   2.017           Gaps:     5
Percent Similarity: 61.702 Percent Identity: 33.333

alignment_block:
US-08-816-01LC-2 x AA464375 ..

Align seg 1/1 to: AA464375 from: 1 to: 401

58 AsnThrTrpThrGlnAspGluIleLeuGlnArgIleSerAspTyrCysAs 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
9 AATTGCGACGGACTGGTAGTAAGTCTCATTCAGCAAAATAGTGGCAGCAATAA 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 pLys.....ProValThrLeuProProThrThrTyrrAspAspThrProt 88
TGCAGGGATTATACGGTTAGAAACACCTCCAATCAATCAGT..... 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
88 yrThrTrpThrPheTyrHisAlaPhePheAlaPheThrValCysSer 104
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ..CACTGGGAVTTGGGAAGTTCCCTCTCTTGCTGGCACCTGTTATTACA 148
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
105 ThrValGlyTyrGlyAsnIleSerProThrThrPheAlaGlyArgMetIl 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
149 ACCATAGGATTTGGAAACATCTACCACGCACAGAAGCGGCAAAATATT 198
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 eMetIleAlaTyrServalIleGlyIleProValAsnGlyIleLeuPheA 138
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 CTGTATCATCTATGCCTTACTTGGGAATTCCTCTTTGGTTTCTCTTGG 248
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
138 laGly.....LeuGlyGluTyrPheGlyArgThrPheGluAla 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 CTGGAGTTGGAGATCAGTCAGTCAGCACCATATTGGAAAAAGGAATTGCCAAA 298
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 IleTyrArgArgTyrLysTyrLysMetSerThrAspMethHisTyrVa 167
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
299 GTGAAGATACGCTTTATTAACTGGAACTTTAGT..... 331
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
167 lProProGlnLeuGlyLeuIleThrThrValIleAlaLeuIleProG 184
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
332 .CAGACCAAGATTGCGATCATCTCAACAATCATATTTATATACTATT...G 377
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 lyIleAlaLeuPheLeuValLeu 191
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 GCTGTGTAAGTCTTTGTGGCTCTG 400
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

seq_name: gb_est47:AW644141

seq_documentation_block:
LOCUS AW644141 632 bp mRNA EST 03-APR-2000
DEFINITION cm37h06.w1 Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0136H06 5', mRNA sequence.
ACCESSION AW644141
VERSION AW644141.1 GI:7401517
KEYWORDS EST.
SOURCE African clawed frog.
```


COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1001032

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 519.

FEATURES

source

```
1. .676
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2136356"
/clone_lib="Sugano mouse kidney mkla"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGG); Site_2: DraIII (CACCATGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGG, 3' site CACCATGG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGGTGG and 3' end
primer CCACCTGCAGCTCGACACA."
```

BASE COUNT 94 a 216 c 211 g 153 t 2 others
ORIGIN

alignment_scores:

Quality: 170.00 Length: 190
Ratio: 1.604 Gaps: 6
Percent Similarity: 55.789 Percent Identity: 27.895

alignment_block:

US-08-816-011C-2 x AI956401 ..

Align seg 1/1 to: AI956401 from: 1 to: 676

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9 LeuLeuIlePheTyrIleSerTyrLeuMetPheGlyAlaAlaIleTyrTy 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 CTGGTGTGGGCTACCTGCTCTACCTGGTGTTCGGCGCGGTCTTCTC 180
25 rHisIleGluHisGlyGluGluLysIleSerArgAlaGluGlnArgLysA 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 GTCCGTGGAGCTGCTTATGAGGACCTGCTGCCGAGGAGCTGGCAAG. 229
42 laGlnIleAlaIleAsnGlnTyrIleLeuGluGluLeuGlyAspLysAsn 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
230 .....CTGAAGCGGCGCTCTCGAGGAGGACGAGGAGCTGCTGCG 268
59 ThrThrThrGlnAspGluIleGlnArgIleSerAspTyrCysAspLy 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 GAGCGGACGCTGGAGCAGTCTCTGGCGCGCTGCTGGAGGCCAGCAATTA 318
75 sProValThrLeuProProThrTyrAspThrProThrThrThrThr 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
319 TGGAGTGTGCTGCTCGACCAACGCTCGGGAAT...TGGAAATGGGACT 365
92 heTyrHisAlaPhePhePheAlaPheThrValCysSerThrValGlyTyr 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
366 TCACCTGGCGCTCTTCTTCGCCAGCACCGGTCTCTCCACCACAGGCTAT 415
```

```
109 GlyAsnIleSerProThrThrPheAlaGlyArgMetIleMetIleAlaTy 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 GGCCACACGGTGCCTCTCAGATGGGGCAAGCCTTCTGCATCATCTA 465
125 rSerValIleGlyIleProValAsnGlyIleLeuPheAlaGlyLeuGlyG 142
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
466 CTCTGTCTATCGGCATCCCGTTTCAAC...CTCCTCTTC..... 499
142 luTyrPheGlyArgThrPheGluAlaIleTyrArgTyrIleTyrLysTy 158
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
500 .....CTGACGGCGGTGGTCCACGCTGTACCGTGCAT 532
159 LysMetSerThrAspMetHisTyrValProGlnLeuGlyLeu..... 173
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
533 GTCACCCCGCAGACCATCTCTACTTCCACATACGCTGNGGCTTCTCAA 582
174 ....IleThrThrValIleAlaLeuIleProGly.....IleA 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
583 GCAGGTGGTGGCCATTGTCCATGCGGTTCTGCTGCTGATTTGTACCGTT 632
186 laLeuPheLeuValLeuPro 192
|||||:|||||:|||||:|||||:|||||:|||||:
633 CCTGCTTCTTCTTCATCCCC 652
```